

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 18:30:15 ; Search time 38 Seconds
(without alignments)
27.852 Million cell updates/sec

Title: US-10-088-681-1
Perfect score: 60
Sequence: 1 TGSFFSELMWTS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 1328

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_79:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	30	50.0	10	2	C39191	hypothetical prote
2	24	40.0	7	2	PHI602	Ig H chain V-D-J r
3	23	38.3	10	2	T13838	cytochrome-c oxida
4	20	33.3	6	2	B34835	dhna protein - Pse
5	20	33.3	11	2	S05002	corazonin - Americ
6	19	31.7	6	2	PT0519	T-cell receptor be
7	19	31.7	6	2	A43129	neuropeptide GMPFR
8	19	31.7	8	2	A41117	acetylcholinestera
9	19	31.7	9	2	S36850	Ig heavy chain V r
10	18	30.0	9	2	S07241	litorin - Rohde's
11	18	30.0	10	2	C41946	T-cell receptor ga
12	18	30.0	10	2	S53789	neuropeptide Pec-H
13	18	30.0	11	1	LPTWWS	probable trpEG lea
14	18	30.0	11	1	S33300	probable substance
15	17.5	29.2	8	2	JS0315	leucokinin V - Mad
16	17	28.3	7	2	PT0586	T-cell receptor be
17	17	28.3	8	2	A44960	neuropeptide led-C
18	17	28.3	8	2	S08995	hypertrehalosemic
19	17	28.3	8	2	A49823	adipokine hormo
20	17	28.3	8	2	A43976	hypertrehalosemic
21	17	28.3	8	2	B43976	hypertrehalosemic
22	17	28.3	8	2	A05169	neuropeptide M-I -
23	17	28.3	10	2	A31571	hypertrehalosemic/
24	16	26.7	4	2	PT0661	T-cell receptor be
25	16	26.7	7	4	I55382	hypothetical pepti
26	16	26.7	8	2	A32523	peptidyl-dipeptida
27	16	26.7	8	2	S11545	adipokine hormo
28	16	26.7	8	2	A61348	red pigment-concen
29	16	26.7	8	2	A28004	adipokine hormo

30	16	26.7	8	2	A39308	glycine reductase
31	16	26.7	9	2	A24244	adipokine hormo
32	16	26.7	9	2	PT0315	Ig heavy chain CRD
33	16	26.7	9	2	A43848	cell surface adhes
34	16	26.7	10	2	S08997	hypertrehalosemic
35	16	26.7	10	2	A60421	hypertrehalosemic
36	16	26.7	10	2	S08998	hypertrehalosemic
37	16	26.7	10	2	A26381	hypertrehalosemic
38	16	26.7	10	2	PT0322	Ig heavy chain CRD
39	16	26.7	10	2	T13976	cytochrome-c oxida
40	16	26.7	10	2	T17057	cytochrome-c oxida
41	16	26.7	10	2	T12303	cytochrome-c oxida
42	16	26.7	10	2	T14019	cytochrome-c oxida
43	16	26.7	10	2	T17060	cytochrome-c oxida
44	16	26.7	10	2	T14043	cytochrome-c oxida
45	16	26.7	10	2	T14054	cytochrome-c oxida
46	16	26.7	10	2	T17066	cytochrome-c oxida
47	16	26.7	10	2	T17069	cytochrome-c oxida
48	16	26.7	10	2	T12308	cytochrome-c oxida
49	16	26.7	10	2	T17072	cytochrome-c oxida
50	16	26.7	10	2	T12312	cytochrome-c oxida
51	16	26.7	10	2	T12316	cytochrome-c oxida
52	16	26.7	10	2	T12321	cytochrome-c oxida
53	16	26.7	10	2	T14219	cytochrome-c oxida
54	16	26.7	11	2	C53652	rhlr protein - Pse
55	16	26.7	11	2	PT0302	Ig heavy chain CRD
56	15	25.0	6	2	B61542	variant surface gl
57	15	25.0	8	2	S10596	adipokine hormo
58	15	25.0	8	2	B27867	homeotic protein U
59	15	25.0	8	2	I48934	apolipoprotein A-I
60	15	25.0	9	2	PT0231	Ig heavy chain CDR
61	15	25.0	9	2	G41946	T-cell receptor ga
62	15	25.0	9	2	T00914	MHC class I histoc
63	15	25.0	10	2	E49033	T-cell receptor ga
64	15	25.0	10	2	E49033	T-cell receptor ga
65	15	25.0	10	2	B61512	variant surface gl
66	15	25.0	10	2	H60588	sperm-activating p
67	15	25.0	11	2	B49164	chromogranin-B - r
68	15	25.0	11	2	PC2372	SRK heat shock pro
69	15	25.0	11	2	A61512	variant surface gl
70	14	23.3	5	2	PT0281	Ig heavy chain CRD
71	14	23.3	5	2	PT0308	Ig heavy chain CRD
72	14	23.3	6	2	A31263	dihydrofolate redu
73	14	23.3	6	2	B31263	dihydrofolate redu
74	14	23.3	7	2	PN0649	pullulanase (EC 3.
75	14	23.3	8	2	B44960	neuropeptide led-C
76	14	23.3	8	2	S08996	hypertrehalosemic
77	14	23.3	8	2	B49823	adipokine hormo
78	14	23.3	8	2	A38887	T-cell receptor ga
79	14	23.3	8	2	A61467	penalbumin - Adeli
80	14	23.3	9	2	C24180	fibritrogen beta ch
81	14	23.3	9	2	PT0288	Ig heavy chain CRD
82	14	23.3	9	2	PT0299	Ig heavy chain CRD
83	14	23.3	9	2	S56004	glucan 1,3-beta-gl
84	14	23.3	9	2	PC7074	translactin elonga
85	14	23.3	10	2	UC1416	hypertrehalosemic
86	14	23.3	10	2	S09138	hypertrehalosemic
87	14	23.3	10	2	UN0024	neurokinin A - chi
88	14	23.3	10	2	A49187	gonadotropin-relea
89	14	23.3	10	2	PT0289	Ig heavy chain CRD
90	14	23.3	10	2	S23370	T-cell receptor al
91	14	23.3	10	2	B49581	T-cell receptor al
92	14	23.3	10	2	A49581	siatokin II - ye
93	14	23.3	10	2	A54348	siatokin II - yel
94	13.5	22.5	10	2	PH0916	N-acetylglucosamin
95	13.5	22.5	10	2	B35640	T-cell receptor be
96	13	21.7	6	2	F41946	cerebellar degener
97	13	21.7	6	2	A41946	T-cell receptor ga
98	13	21.7	7	2	S09652	hypothetical prote
99	13	21.7	7	2	PT0628	T-cell receptor be
100	13	21.7	7	2	S33567	tubulin beta-3 cha

ALIGNMENTS

RESULT 1

C39191
hypothetical protein 1 (Tetx 5' region) - Bacteroides fragilis
C/Species: Bacteroides fragilis
C/Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 30-Sep-1993
C/Accession: C39191
R/Speer, B.S.; Badzyk, L.; Salyers, A.A.
J. Bacteriol. 173, 176-183, 1991
A/Title: Evidence that a novel tetracycline resistance gene found on two Bacteroides tra
A/Reference number: A39191; MUID:91100280; PMID:1846135
A/Accession: C39191
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-10 <SP>
A/Cross-references: GB:M37699

Query Match 50.0%; Score 30; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 19;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 FSELMWTS 11
: || ||
Db 2 YFSRPWTS 9

RESULT 2

PH1602
Ig H chain V-D-J region (wild-type clone 313) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C/Accession: PH1602
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A/Title: Molecular characterization of transgene-induced immunodeficiency in B-1ess mice

A/Reference number: PH1580; MUID:93301609; PMID:8315387

A/Accession: PH1602

A/Molecule type: DNA

A/Residues: 1-7 <LEV>

A/Experimental source: bone marrow pre-B lymphocyte

C/Keywords: immunoglobulin

Query Match 40.0%; Score 24; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 SELMT 10
: || ||
Db 3 SSLMT 7

RESULT 3

TI1838
cytochrome-c oxidase (EC 1.9.3.1) chain I - Bipos biporus mitochondrion (fragment)

C/Species: mitochondrion Bipos biporus

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C/Accession: TI1838

R/Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.

Mol. Biol. Evol. 14, 91-104, 1997

A/Title: Two novel gene orders and the role of light-strand replication in rearrangement

A/Reference number: Z17789; MUID:9155826; PMID:9000757

A/Accession: TI1838

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-10 <MAC>

A/Cross-references: UNIPROT:P92576; EMBL:U71335; NID:g1753232; PID:g1753235; PIDN:AA482

C/Genetics: A/Genome: mitochondrion
A/Note: COI
C/Keywords: mitochondrion; oxidoreductase

Query Match 38.3%; Score 23; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGSFPS 6
: || ||
Db 4 TRSFFS 9

RESULT 4

B34835
dnaA protein - Pseudomonas aeruginosa (fragment)

C/Species: Pseudomonas aeruginosa

C/Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999

C/Accession: B34835

R/Yee, T.W.; Smith, D.W.

Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990

A/Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from Bac

A/Reference number: A34835; MUID:90160310; PMID:2106132

A/Accession: B34835

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-6 <YEE>

A/Cross-references: GB:M30125; NID:g151419; PIDN:AAA25916.1; PID:g151421

Query Match 33.3%; Score 20; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ELW 9
: || ||
Db 4 ELW 6

RESULT 5

S05002
corazonin - American cockroach

C/Species: Periplaneta americana (American cockroach)

C/Date: 07-Sep-1990 #sequence_revision 09-Apr-1998 #text_change 09-Jul-2004

C/Accession: S05002

R/Venestra, J.A.

FEBS Lett. 250, 231-234, 1989

A/Title: Isolation and structure of corazonin, a cardioactive peptide from the american c

A/Reference number: S05002; MUID:89355572; PMID:2753132

A/Accession: S05002

A/Molecule type: Protein

A/Residues: 1-11 <VEE>

A/Cross-references: UNIPROT:P11496

C/Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:1/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 33.3%; Score 20; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 1.4e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 FSELMWTS 11
: || ||
Db 5 YSRGWTW 11

RESULT 6

PT0519
T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C/Accession: PT0519

R/Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A/Reference number: PT0509; MUID:91277601; PMID:1711558
A/Accession: PT0519

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-6 <FE>
A:Experimental source: adult thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 31.7% Score 19; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 SELW 9
: : :
: : :
Db 2 SELW 5

RESULT 7
A43129
neuropeptide GNFRFamide - tapeworm (Montezia expansa)

C:Species: Montezia expansa

C:Date: 10-Nov-1997 #sequence_revision 14-Nov-1997 #text_change 09-Jul-2004

C:Accession: A43129

R:Maule, A.; Shaw, C.; Halton, D.; Thim, L.

Biochem. Biophys. Res. Commun. 193, 1054-1060, 1993

A:Title: GNFRFamide: A novel FMRFamide-immunoreactive peptide isolated from the sheep

A:Reference number: A43129; MUID:93312289; PMID:8323531

A:Accession: A43129

A:Molecule type: protein

A:Residues: 1-6 <MAU>

A:Cross-references: UNIPROT:P41966

C:Keywords: amidated carboxyl end; neuropeptide

F:6/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 31.7% Score 19; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSFP 5
: : :
: : :
Db 1 GNFP 4

RESULT 8
A41117
acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)

C:Species: Naja naja oxiana (Asian cobra, Oxis cobra)

C:Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004

C:Accession: A41117

R:Kreienkamp, H.J.; Weise, C.; Raba, R.; Aavikkaar, A.; Huch, F.

Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991

A:Title: Amino acid substrates of the catalytic center of acetylcholinesterase from Torpedo

A:Reference number: A41117; MUID:91296772; PMID:2068091

A:Accession: A41117

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <KRB>

A:Cross-references: UNIPROT:Q7LZ27

C:Keywords: carboxylic ester hydrolase

Query Match 31.7% Score 19; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 SELW 9
: : :
: : :
Db 2 AEMW 5

RESULT 9
S36850

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999

C:Accession: S36850

R:Jacob, J.; Kelsse, G.

Submitted to the EMBL Data Library, July 1992

A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl)

A:Reference number: S25024

A:Accession: S36850

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-9 <UAC>

A:Cross-references: EMBL:X67387; NID:950113; PIDN:CAA47799.1; PID:es1594; PID:q1333871

C:Keywords: heterotrimer; immunoglobulin

Query Match 31.7% Score 19; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSFP 5
: : :
: : :
Db 6 GSFP 9

RESULT 10
S07241

litorin - Rohde's leaf frog

C:Species: Phyllomedusa rohdei (Rohde's leaf frog)

C:Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004

C:Accession: S07241

R:Barra, D.; Falconieri Erspamer, G.; Simmaco, M.; Borea, F.; Melchiorri, P.; Erspamer, V.

FEBS Lett. 182, 53-56, 1985

A:Title: Rohdei-litorin: a new peptide from the skin of Phyllomedusa rohdei.

A:Reference number: S07241; MUID:55127560; PMID:3838283

A:Accession: S07241

A:Molecule type: protein

A:Residues: 1-9 <BAR>

A:Cross-references: UNIPROT:P08946

C:Superfamily: gastrin-releasing peptide

C:Keywords: amidated carboxyl end; blocked amino end; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 30.0% Score 18; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 ELWTS 11
: : :
: : :
Db 1 OLWAT 5

RESULT 11
C41946

T-cell receptor gamma chain (lt.60) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: C41946

R:Wheatsell, M.; Mosley, R.L.; Wheatsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ger

A:Reference number: A41946; MUID:92049316; PMID:1658619

A:Accession: C41946

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-10 <WHR>

C:Keywords: T-cell receptor

Query Match 30.0% Score 18; DB 2; Length 10;
Best Local Similarity 28.6%; Pred. No. 2.9e+03;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 FSELWTS 11
: : :
: : :
Db 1 YCAVWSS 7

RESULT 12

SS3789
neuropeptide Peg-HrTH - Platypleura capensis
C/Species: Platypleura capensis
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: SS3789
R/Gade, G.; Janssens, M.P.E.
Biol. Chem. Hoppe-Seyler 375, 803-809, 1994
A/Title: Cicadas contain novel members of the AKG/RPCH family peptides with hypertrehalose
A/Reference number: SS3789; MUID:95225985; PMID:7710694
A/Accession: SS3789
A/Molecule type: protein
A/Residues: 1-10 <GAE>
A/Cross-references: UNIPROT:Q7M465
C/Keywords: blocked amino end; blocked carboxyl end

Query Match 30.0%; Score 18; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GSELM 9
DB 4 GSPSW 8

RESULT 13

LEFTWME

probable trpEG leader peptide - Thermus aquaticus

C/Species: Thermus aquaticus
C/Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C/Accession: S03315
R/Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.
Biochim. Biophys. Acta 950, 303-312, 1988
A/Title: Molecular cloning and nucleotide sequence of Thermus thermophilus HB8 trpE and
A/Reference number: S03315; MUID:89000781; PMID:2844259
A/Accession: S03315
A/Molecule type: DNA
A/Residues: 1-11 <SAT>
A/Cross-references: EMBL:X07744; NID:948261; PIDN:CA30565.1; PID:948262
A/Note: the source is designated as Thermus thermophilus HB8
C/Genetics:
A/Gene: trpL
C/Superfamily: probable trpEG leader peptide

Query Match 30.0%; Score 18; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 SELW 9
DB 5 SALW 8

RESULT 14

S33300

probable substance P - smaller spotted catshark

C/Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S33300
R/Maugh, D.; Wang, Y.; Hazon, N.; Baiment, R.J.; Conlon, J.M.
Eur. J. Biochem. 214, 469-474, 1993
A/Title: Primary structures and biological activities of substance-P-related peptides fr
A/Reference number: S33300; MUID:93292508; PMID:7685693
A/Accession: S33300

A/Molecule type: protein
A/Residues: 1-11 <WAU>
A/Cross-references: UNIPROT:P41333
A/Experimental source: brain
C/Function:

A/Description: may play a physiological role in the regulation of cardiovascular and gas
A/Note: substance P is derived by post-translational processing of preprotachykinin A
C/Keywords: amidated carboxyl end; neuropeptide; tachykinin
F/1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 30.0%; Score 18; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSPF 5
DB 5 GQPF 8

RESULT 15

JS0315

leucokinin V - Madeira cockroach

C/Species: Leucophaea maderae (Madeira cockroach)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C/Accession: JS0315
R/Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 27-30, 1987
A/Title: Isolation, primary structure, and synthesis of leucokinin V and VI: myotropic
A/Reference number: JS0315
A/Accession: JS0315
A/Molecule type: protein
A/Residues: 1-8 <HOL>
A/Cross-references: UNIPROT:P19987
C/Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile acti
C/Keywords: amidated carboxyl end; cephalomyotropic peptide
F/8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 29.2%; Score 17.5; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 2.8e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 2 GSPFSELW 9
DB 1 GSGPFS-W 7

Search completed: August 3, 2005, 18:41:43
Job time : 40 secs

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OM protein - protein search, using sw model

Run on: August 3, 2005, 18:18:34 ; Search time 166 Seconds

(without alignments)
33.933 Million cell updates/sec

Title: US-10-088-681-1
Perfect score: 60
Sequence: 1 TGSFFSFLMTS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3223

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	24	40.0	11 2 077895	077895 oreochromis
2	24	40.0	11 2 077896	077896 oreochromis
3	23	38.3	10 2 P92576	P92576 bipes bipor
4	23	38.3	11 2 P83537	P83537 lactobacilli
5	21	35.0	9 2 O95953	O95953 homo sapien
6	20	33.3	10 2 O61A62	O61A62 homo sapien
7	20	33.3	11 1 CA42_LITCI	CA42_LITCI
8	20	33.3	11 1 COR2_PERAM	COR2_PERAM
9	20	33.3	11 2 077894	077894 oreochromis
10	20	33.3	11 2 077898	077898 oreochromis
11	20	33.3	11 2 O65CG7	O65CG7 sinaloa tom
12	19	31.7	6 1 PARP_MONEX	PARP_MONEX
13	19	31.7	8 2 O99MNO	O99MNO mus musculu
14	19	31.7	8 2 Q7L227	Q7L227 naja oxiata
15	19	31.7	10 2 Q9TR47	Q9TR47 bos taurus
16	19	31.7	10 2 O6SHC6	O6SHC6 furcifer be
17	19	31.7	11 2 O9UC46	O9UC46 homo sapien
18	18	30.0	9 1 LITR_PHYRO	LITR_PHYRO
19	18	30.0	9 2 O9H3Y3	O9H3Y3 homo sapien
20	18	30.0	9 2 O6H9Z1	O6H9Z1 cyonophaga
21	18	30.0	9 2 O90350	O90350 gp virus c/
22	18	30.0	10 1 AKHX_LOCM1	AKHX_LOCM1
23	18	30.0	10 2 Q7M465	Q7M465 platypieura
24	18	30.0	10 2 O6SHB1	O6SHB1 rhampoleon
25	18	30.0	10 2 O6SHB4	O6SHB4 furcifer ve
26	18	30.0	10 2 O6SHB7	O6SHB7 furcifer ou
27	18	30.0	10 2 O6SHC0	O6SHC0 furcifer la
28	18	30.0	10 2 O6SHC3	O6SHC3 thermus the
29	18	30.0	11 1 LPW_THETH	LPW_THETH
30	18	30.0	11 1 TKNA_SCYCA	TKNA_SCYCA
31	18	30.0	11 2 Q9UE10	Q9UE10 homo sapien

32	17.5	29.2	8	1	LCK5_LEUMA	P19987 leucophaea
33	17.5	29.2	11	2	O9G5Z2	O9G5Z2 pseudocalot
34	17	28.3	8	1	HTE1_PERAM	HTE1_PERAM
35	17	28.3	8	1	HTE_TENMO	HTE_TENMO
36	17	28.3	8	1	HTE_ZOPRU	HTE_ZOPRU
37	17	28.3	8	2	O40530	O40530 nicotiana t
38	17	28.3	9	2	O8WGE6	O8WGE6 procambarus
39	17	28.3	10	1	HTE_HELZE	HTE_HELZE
40	17	28.3	10	1	LABA_JATMU	LABA_JATMU
41	17	28.3	10	2	O9TUJ3	O9TUJ3 canis famli
42	17	28.3	10	2	O7J505	O7J505 ovis aries
43	17	28.3	11	1	CA22_LITCI	CA22_LITCI
44	17	28.3	11	1	MBBI_KLEBN	MBBI_KLEBN
45	17	28.3	11	2	O90735	O90735 gallus galli
46	17	28.3	11	2	O9P664	O9P664 gallus galli
47	16	26.7	5	1	PAP2_PARMA	PAP2_PARMA
48	16	26.7	6	1	E101_LITRU	E101_LITRU
49	16	26.7	8	1	AKHG_GRYBI	AKHG_GRYBI
50	16	26.7	8	1	AKH_PROTE	AKH_PROTE
51	16	26.7	8	1	AKH_ROMMI	AKH_ROMMI
52	16	26.7	8	1	RPCH_PANBO	RPCH_PANBO
53	16	26.7	8	2	O7M3E2	O7M3E2 bos taurus
54	16	26.7	8	2	O94PX5	O94PX5 felis silve
55	16	26.7	8	2	O94PX6	O94PX6 felis libyc
56	16	26.7	8	2	O94PX7	O94PX7 felis silve
57	16	26.7	8	2	O94VA7	O94VA7 varanus sal
58	16	26.7	8	2	O94VB2	O94VB2 varanus sal
59	16	26.7	8	2	O94VB5	O94VB5 varanus sal
60	16	26.7	8	2	O70Y57	O70Y57 fueretia af
61	16	26.7	8	2	O7M0L0	O7M0L0 clostridium
62	16	26.7	8	2	O7X145	O7X145 streptolocc
63	16	26.7	8	2	O99NX9	O99NX9 hydrocoeru
64	16	26.7	8	2	O62721	O62721 ratius norv
65	16	26.7	9	2	AKH_HELZE	AKH_HELZE
66	16	26.7	9	2	O9MMA3	O9MMA3 homo sapien
67	16	26.7	9	2	O94VC6	O94VC6 varanus pil
68	16	26.7	9	2	O691D6	O691D6 anolis sagr
69	16	26.7	9	2	O9TE68	O9TE68 gecko gecko
70	16	26.7	9	2	O98366	O98366 bacterioph
71	16	26.7	9	2	O9R5M1	O9R5M1 staphylococ
72	16	26.7	9	2	O673W5	O673W5 tyranus me
73	16	26.7	9	2	O673W6	O673W6 terpsiphon
74	16	26.7	9	2	O673W7	O673W7 telophorus
75	16	26.7	9	2	O673W8	O673W8 tchagra sen
76	16	26.7	9	2	O673W9	O673W9 tchagra aus
77	16	26.7	9	2	O673X0	O673X0 rhodophonu
78	16	26.7	9	2	O673X1	O673X1 rhididura a
79	16	26.7	9	2	O673X2	O673X2 pseudobias
80	16	26.7	9	2	O673X3	O673X3 prionops sc
81	16	26.7	9	2	O673X4	O673X4 prionops re
82	16	26.7	9	2	O673X5	O673X5 platystelea
83	16	26.7	9	2	O673X6	O673X6 oriolus xan
84	16	26.7	9	2	O673X7	O673X7 nillaus afer
85	16	26.7	9	2	O673X8	O673X8 bias flammu
86	16	26.7	9	2	O673X9	O673X9 malaconotus
87	16	26.7	9	2	O673Y0	O673Y0 lanius coli
88	16	26.7	9	2	O673Y1	O673Y1 lanioturdus
89	16	26.7	9	2	O673Y2	O673Y2 laniarius f
90	16	26.7	9	2	O673Y3	O673Y3 laniarius f
91	16	26.7	9	2	O673Y4	O673Y4 laniarius b
92	16	26.7	9	2	O673Y5	O673Y5 laniarius b
93	16	26.7	9	2	O673Y6	O673Y6 platystelea
94	16	26.7	9	2	O673Y7	O673Y7 dyoscopus
95	16	26.7	9	2	O673Y8	O673Y8 dyoscopus
96	16	26.7	9	2	O673Y9	O673Y9 dicrurus pa
97	16	26.7	9	2	O673Z0	O673Z0 cyanolanius
98	16	26.7	9	2	O673Z1	O673Z1 corvus coro
99	16	26.7	9	2	O673Z2	O673Z2 coracina me
100	16	26.7	9	2	O673Z3	O673Z3 telophorus

ALIGNMENTS

RESULT 1

077895 PRELIMINARY; PRT; 11 AA.
ID 077895
AC 077895
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Perciformes; Labroidel;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
R Figueira F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
class II B loci";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050005; AAC4134.1; -.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1367 MW; 3F47C9EA72045A3 CRC64;
Query Match 40.0%; Score 24; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 2

077896 PRELIMINARY; PRT; 11 AA.
ID 077896
AC 077896
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Perciformes; Labroidel;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
R Figueira F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
class II B loci";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050006; AAC41345.1; -.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1399 MW; 3F47DB7A772685A3 CRC64;
Query Match 40.0%; Score 24; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 3

P92576 PRELIMINARY; PRT; 10 AA.
ID P92576
AC P92576
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
OS Name=COL;
GN Bipes biporus (Baja worm lizard).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Amphisbaenia; Bipedidae; Bipes.
OX NCBI_TaxID=52188;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153826; PubMed=9000757;
RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
RT "Two novel gene orders and the role of light-strand replication in
rearrangement of the vertebrate mitochondrial genome";
RL Mol. Biol. Evol. 14:91-104(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153820; PubMed=9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
structures of mitochondrial transfer RNAs";
RL Mol. Biol. Evol. 14:30-39(1997).
DR EMBL; U71335; AA848271.1; -.
DR PIR; T13838; T13838.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1176 MW; 5B3580C9D5A411A7 CRC64;

Query Match 38.3%; Score 23; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.7e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 4

P83537 PRELIMINARY; PRT; 11 AA.
ID P83537
AC P83537
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE AND INDUCTION.
RC STRAIN=DSM 20451;
RX PubMed=12112860;
DOI=10.1002/1615-9861(200206)2:6<765::AID-PROT765>3.0.CO;2-V;
RA Drews O., Weiss W., Reil G., Parlar H., Wält R., Goerg A.;
RT "High pressure effects step-wise altered protein expression in
Lactobacillus sanfranciscensis";
RL Proteomics 2:765-774(2002).
CC -1- INDUCTION: By elevated hydrostatic pressure.
CC -1- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
protein is: 65 kDa.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1249 MW; D96C8231B771ADD9 CRC64;

Query Match 38.3%; Score 23; DB 2; Length 11;

Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 GSFFS 6
Db 1 GSFFA 5

RESULT 5

095953 PRELIMINARY; PRT; 9 AA.
AC 095953;
DT 01-MAY-1999 (TRENBLREL. 10, Created)
DT 01-MAY-1999 (TRENBLREL. 10, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Galactocerebrosidase (EC 3.2.1.46) (Fragment).
GN Name=GALC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Lull L., Torchiana E., Finocchiaro G.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U77631; AAD15626.1; -;
DR GO; GO:0004336; F:galactosylceramidase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
KW Glycosidase; Hydrolase.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1069 MW; 374E2AADC2C699C8 CRC64;
Query Match 35.0%; Score 21; DB 2; Length 9;
Best Local Similarity 37.5%; Pred. No. 1.6e+06;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 GSFFSELM 9
Db 2 GFVAVADLM 9

RESULT 6
061A62 PRELIMINARY; PRT; 10 AA.
AC 061A62;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Amloride-sensitive epithelial sodium channel gamma subunit (Fragment).
GN Name=SCNN1G;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96421599; PubMed=8824247; DOI=10.1074/jbc.271.42.26062;
RA Thomas C.P., Doggett N.A., Fisher R., Stokes J.B.;
RT "Genomic organization and the 5' flanking region of the gamma subunit of the human amloride-sensitive epithelial sodium channel.";
RT J. Biol. Chem. 271:26062-26066 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98316780; PubMed=9654208;
RA Ludwig M., Bolkenius U., Wiekert L., Marynen P., Bidlingmaier F.;
RT "Structural organization of the gene encoding the alpha-subunit of the human amloride-sensitive epithelial sodium channel.";
RT Hum. Genet. 102:576-581 (1998).
DR EMBL; Z92982; CAB07506.1; -;
DR GO; GO:0005216; F:ion channel activity; IEA.

KW Ionic channel.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1157 MW; DBAEF833733B05A2 CRC64;

Query Match 33.3%; Score 20; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 9.1e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 SFSELM 9
Db 1 SVSEKX 7

RESULT 7

CA42_LITCI STANDARD; PRT; 11 AA.
ID CA42_LITCI
AC P82052;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Caerulein 4.2/4.2Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue mountains tree frog Litoria citropa. Part 1. Sequence determination using electrospray mass spectrometry.";
RT Rapid Commun. Mass Spectrom. 13:2498-2502 (1999).
CC -1- FUNCTION: Hypoensitive neuropeptide (Probable).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin dorsal glands.
CC -1- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being sulfated.
CC -1- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray; RANGE=1-11;
NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSB_NEG.
KW Amidation; Amphibian defense peptide; Direct protein sequencing;
KW Hypoensitive agent; Pyrrolidone carboxylic acid; Sulfation.
FT MOD_RRS 1 4
FT MOD_RRS 1 4
FT MOD_RRS 11 11
FT MOD_RRS 11 11
SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;
Query Match 33.3%; Score 20; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TGSFF 5
Db 5 TGSFF 9

RESULT 8
CORZ_PERAM STANDARD; PRT; 11 AA.
ID CORZ_PERAM
AC P11496;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Corazonin.
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattellidae;
OC Blattidae; Periplaneta.

OC NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RA MEDLINE=9932572; PubMed=2753132; DOI=10.1016/0014-5793(89)80727-6;
RX Venesira J.A.;
RT "Isolation and structure of corazonin, a cardioactive peptide from the
American cockroach";
RL FBS let. 250:231-234(1989).
CC -1- FUNCTION: Cardioactive peptide. Corazonin is probably involved in
the physiological regulation of the heart beat.
CC -1- SUBCELLULAR LOCATION: Secreted.
DR PIR; S05002; S05002.
KM Annotation: Direct protein sequencing; Neuropeptide;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 Asparagine amide.
FT MOD_RES 11 11 Asparagine amide.
SQ SEQUENCE 11 AA; 1387 MW; C7CFE32D6415AB46 CRC64;

Query Match 33.3%; Score 20; DB 1; Length 11;
Best Local Similarity 42.9%; Pred. No. 1e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 FSELMTS 11
Db 5 YSRGWTN 11

RESULT 9
077894 PRELIMINARY; PRT; 11 AA.

ID 077894
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=9831513; PubMed=9649539;
RA Melaga-Tillio E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueira F., Sultmann H., Klein U.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050004; AAC41343.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;

Query Match 33.3%; Score 20; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 FSELM 9
Db 3 FMSIWM 8

RESULT 10
077898 PRELIMINARY; PRT; 11 AA.
AC 077898
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9831513; PubMed=9649539;
RA Melaga-Tillio E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueira F., Sultmann H., Klein U.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050008; AAC41347.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;

Query Match 33.3%; Score 20; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 FSELM 9
Db 3 FMSIWM 8

RESULT 11
065CG7 PRELIMINARY; PRT; 11 AA.

ID 065CG7
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Transcriptional activator (Fragment).
GN Name=AC2;
OS Sinlao tomato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=71166;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NT3;
RA Rojas A., Kvarnheden A., Rodriguez D., Valkonen J.P.T.;
RT "A mixture of begomoviruses in severe leaf curl-affected tomatoes in
Nicaragua.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ508781; CAD48523.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1356 MW; 861BC90602D379D5 CRC64;

Query Match 33.3%; Score 20; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1e+04;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 SPFSELM 10
Db 4 SPFWELFS 11

RESULT 12
FARP MONEX STANDARD; PRT; 6 AA.
ID FARP MONEX
AC P41966;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRFamide-like neuropeptide GNFRF-amide.
OS Moniezia expansa (Sheep tapeworm).
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Anoplocephalidae; Moniezia.
OX NCBI_TaxID=28841;
RN [1]
RP SEQUENCE.

RX MEDLINE=93312289; PubMed=8323531;
RA Maule A.G., Shaw C., Halton D.W., Thim L.;
RT "GNFRFamide: a novel FMRFamide-immunoreactive peptide isolated from
RL the sheep tapeworm, Moniezia expansa.";
RL Blochem. Biophys. Res. Commun. 193:1054-1060(1993).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the PARP (FMRFamide related peptide)
family.
DR PIR; A43129; A43129.
KM Annotation: Direct protein sequencing; Neuropeptide.
FT MOD_RSS 6 Phenylalanine amide.
SQ SEQUENCE 6 AA; 787 MW; 69D409C9C448100 CRC64;

Query Match 31.7%; Score 19; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSFF 5
DB 1 GNFF 4

RESULT 13
ID 099MNO PRELIMINARY; PRT; 8 AA.
AC 099MNO;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Adenosine deaminase tRNA-specific 1 (Fragment).
GN Name:Adact1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Svj;
RX MEDLINE=21231131; PubMed=11331948;
RA Maas S., Kim Y.G., Rich A.;
RT "Genomic clustering of tRNA-specific adenosine deaminase ADAT1 and two
RT tRNA synthetases.";
RL Mamm. Genome 12:387-393(2001).
DR EMBL; AF328904; AAK19310.1; -.
DR MGD; MGI:1353631; Adact1.
FT NON_TER 8
SQ SEQUENCE 8 AA; 936 MW; F4D05B1AADCB376 CRC64;

Query Match 31.7%; Score 19; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 LMTS 11
DB 1 MMTA 4

RESULT 14
ID 07LZ27 PRELIMINARY; PRT; 8 AA.
AC 07LZ27;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Acetylcholinesterase (BC 3.1.1.7), venom (Fragment).
OS Naja oxiata (Central Asian cobra) (Oxus cobra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepadousaria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Elapinae; Naja.
OX NCBI_TaxID=8657;
RN [1]
RP SEQUENCE.
RX MEDLINE=91296772; PubMed=2068091;

RA Krienkamp H.J., Weise C., Raba R., Ayikkaar A., Hucho F.;
RT "Anionic subites of the catalytic center of acetylcholinesterase from
RT Torpedo and from cobra venom.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:6117-6121(1991).
DR PIR; A41117; A41117.
DR GO; GO:0003990; F:acetylcholinesterase activity; IEA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 918 MW; 7P576453769B1D8 CRC64;

Query Match 31.7%; Score 19; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 SELW 9
DB 2 AEMW 5

RESULT 15
ID 09TR47 PRELIMINARY; PRT; 10 AA.
AC 09TR47;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Amphoterin homolog (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=96029671; PubMed=7592757; DOI=10.1074/jbc.270.43.25752;
RA Hori O., Brett J., Slattery T., Gao R., Zhang J., Chen J.X.,
RA Nagashima M., Lundh E.R., Vijay S., Nitecki D.;
RT "The receptor for advanced glycation end products (RAGE) is a cellular
RT binding site for amphoterin. Mediation of neurite outgrowth and co-
RT expression of rage and amphoterin in the developing nervous system.";
RL J. Biol. Chem. 270:25752-25761(1995).
SQ SEQUENCE 10 AA; 1163 MW; 28E5034453769B18 CRC64;

Query Match 31.7%; Score 19; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 ELMTS 11
DB 4 EMMN 8

Search completed: August 3, 2005, 18:41:09
Job time : 179 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2005, 18:17:29 ; Search time 161 Seconds
(without alignments)
26.425 Million cell updates/sec

Title: US-10-088-681-1
Perfect score: 60
Sequence: 1 TGSFSELMWS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 494136

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_GeneSeq_16Dec04:*
1: geneeqp1980s:*
2: geneeqp1990s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	56.7	8	3	AAB09130
2	31	51.7	10	8	ADK09671
3	31	51.7	10	8	ADK09188
4	30	50.0	6	6	ABR46515
5	30	50.0	9	2	AAW72493
6	30	50.0	10	2	AAW37198
7	29	48.3	7	2	AAV33139
8	29	48.3	10	5	AAU93215
9	29	48.3	11	6	ABU37125
10	28	46.7	6	6	ABR46459
11	28	46.7	7	8	ADR68302
12	28	46.7	9	2	AAV04678
13	28	46.7	10	4	ABR55959
14	28	46.7	11	3	AAV93379
15	28	46.7	11	7	ADP53467
16	27	45.0	6	2	AAAR8913
17	27	45.0	6	3	AAAB1704
18	27	45.0	6	5	ABR73169
19	27	45.0	6	5	ABR46527
20	27	45.0	6	6	ABR46507
21	27	45.0	6	6	ABG73432
22	27	45.0	6	7	ADU73323
23	27	45.0	6	8	ADU52957
24	27	45.0	6	8	ADU51918
25	27	45.0	6	8	ADU51918

26	27	45.0	7	2	AAR89921
27	27	45.0	7	2	AAR89925
28	27	45.0	7	3	AAV57789
29	27	45.0	8	8	ADQ28799
30	27	45.0	8	8	ADQ28800
31	27	45.0	9	2	AAW37199
32	27	45.0	9	5	AAE31317
33	27	45.0	9	5	AAE31316
34	27	45.0	9	5	AAE31395
35	27	45.0	9	8	ADK09130
36	27	45.0	9	8	ADK09595
37	27	45.0	9	8	ADQ28798
38	27	45.0	9	8	ADP80098
39	27	45.0	10	2	AAR89917
40	27	45.0	10	2	AAW13605
41	27	45.0	10	8	ADG78885
42	27	45.0	10	8	ADN48959
43	27	45.0	10	8	ADN64792
44	27	45.0	10	8	ADP47192
45	27	45.0	10	8	ADQ90923
46	27	45.0	10	8	ADP80344
47	27	45.0	10	8	ADT02867
48	27	45.0	11	2	AAW11231
49	27	45.0	11	4	AAU27152
50	27	45.0	11	4	AAU26842
51	27	45.0	11	5	AAE52269
52	27	45.0	11	8	ADN64806
53	27	45.0	11	8	ADP80368
54	26	43.3	5	2	AAR89912
55	26	43.3	6	6	ABR46403
56	26	43.3	8	6	ABP98083
57	26	43.3	8	6	ABP98084
58	26	43.3	8	6	ABP98081
59	26	43.3	8	6	ABP98082
60	26	43.3	8	8	ADSO0534
61	26	43.3	8	8	ADSO0532
62	26	43.3	8	8	ADSO0533
63	26	43.3	8	8	ADSO0535
64	26	43.3	8	8	ADR99992
65	26	43.3	8	8	ADR99995
66	26	43.3	8	8	ADR99994
67	26	43.3	8	8	ADR99993
68	26	43.3	8	8	ADSS4213
69	26	43.3	8	8	ADSS4215
70	26	43.3	8	8	ADSS4216
71	26	43.3	8	8	ADSS4214
72	26	43.3	10	8	ADG94728
73	26	43.3	10	8	ADL47102
74	26	43.3	10	8	ADP87303
75	25	41.7	5	7	ABG75141
76	25	41.7	6	6	ABR46739
77	25	41.7	6	6	ABR46531
78	25	41.7	6	6	ABR46523
79	25	41.7	6	6	ABR46451
80	25	41.7	6	6	ABR46519
81	25	41.7	7	6	ABR31848
82	25	41.7	8	6	ABR54137
83	25	41.7	8	6	ABR54135
84	25	41.7	8	6	ABR54139
85	25	41.7	8	6	ABR54141
86	25	41.7	8	7	ADP47092
87	25	41.7	8	8	ADL02276
88	25	41.7	9	5	AAU72829
89	25	41.7	9	5	ABG67520
90	25	41.7	9	6	ADL23636
91	25	41.7	9	7	ADL17228
92	25	41.7	9	8	ADK03025
93	25	41.7	10	5	ABG70412
94	25	41.7	10	5	ABU82448
95	25	41.7	10	7	ADK07748
96	25	41.7	10	8	ADP47006
97	25	41.7	10	8	ADP47009
98	25	41.7	10	8	ADP47009

AAR89921	Antibody
AAR89925	p53 bindi
AAV57789	TRAM-inte
ADQ28799	Human cel
ADQ28800	Human cel
AAW37199	Human onc
AAE31317	Human p53
AAE31316	Human p53
AAE31395	Human p53
ADK09130	Human pap
ADK09595	Human pap
ADQ28798	Human cel
ADP80098	Human HLA
AAR89917	Human p53
AAW13605	p53 prote
ADG78885	Human p53
ADN48959	Peptide #
ADN64792	HLA bindi
ADP47192	Human pho
ADQ90923	Pancrreati
ADP80344	Human HLA
ADT02867	Human p53
AAW11231	Peptide A
AAU27152	Human Leu
AAU26842	Human Leu
AAE52269	Miniature
ADN64806	HLA bindi
ADP80368	Human HLA
AAR89912	p53/MDM2
ABR46403	Staphyloc
ABP98083	Amino aci
ABP98084	Amino aci
ABP98081	Amino aci
ABP98082	Amino aci
ADSO0534	Human Apo
ADSO0532	Human Apo
ADSO0533	Human Apo
ADSO0535	Human Apo
ADR99992	Human apo
ADR99995	Human apo
ADR99994	Human apo
ADR99993	Human apo
ADSS4213	Human apo
ADSS4215	Human apo
ADSS4216	Human apo
ADSS4214	Human apo
ADG94728	Human JAM
ADL47102	Permeabil
ADP87303	Human cla
ABG75141	F lacticid
ABR46739	Staphyloc
ABR46531	Staphyloc
ABR46523	Staphyloc
ABR46451	Staphyloc
ABR46519	Staphyloc
ABR31848	Androgen
ABR54137	Beta-secr
ABR54135	Beta-secr
ABR54139	Beta-secr
ABR54141	Beta-secr
ADP47092	YPSI prot
ADL02276	Murine im
AAU72829	Ant-i-NKG2
ABG67520	Human ADP
ADL23636	Alzheimer
ADL17228	Phase-dis
ADK03025	Hepatitlis
ABG70412	CDRI/HLI
ABU82448	Llama CDR
ADK07748	Canine im
ADP47006	Murine he
ADP47009	Murine he

XX WO2004011650-A2.
XX
XX 05-FEB-2004.
XX
XX 24-JUL-2003; 2003WO-EP008112.
XX
XX 24-JUL-2002; 2002AT-00001124.
XX
XX 11-JUL-2003; 2003EP-00450171.
XX
XX (INTE-) INTERCELL AG.
XX
XX Maltner F, Schmidt W, Habel A;
XX
XX WPI; 2004-169243/16.
XX
XX New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.
XX
XX Claim 18; Page 187; 220pp; English.
XX
XX This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
CC invention.
XX
XX Sequence 10 AA;

Query Match 51.7%; Score 31; DB 8; Length 10;
Best Local Similarity 62.5%; Pred. No. 96;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SFPSLMT 10
DB 1 SFPSRTWS 8

RESULT 4
ABR46515
ID ABR46515 standard; peptide; 6 AA.
XX
AC ABR46515;
XX

DT 10-JUN-2003 (first entry)
XX

DE Staphylococcus aureus CHIPS-related peptide #1705.
XX

XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; CSAR;
XX formylated peptide receptor; PPR; neutrophil; monocyte; endothelial cell;
XX inflammation; cardiovascular disease; central nervous system disease;
XX gastrointestinal disease; skin disease; genitourinary disease;
XX joint disease; respiratory disease; HIV infection; antiinflammatory;
XX cardiac; cerebroprotective; neuroprotective; nootropic; dermatological;
XX gynecological; immunosuppressive; anti-HIV.
XX
XX Staphylococcus aureus.
OS
OS Synthetic.
OS

XX WO2003006048-A1.
XX

XX 23-JAN-2003.
XX

XX 11-JUL-2001; 2001WO-EP008004.
XX

XX 11-JUL-2001; 2001WO-EP008004.
XX

XX

PA (JARI-) JARI PHARM BV.
XX
XX Van Kessel CPM, Gosselaar-De Haas CTC, Kruijtzler JMW;
PI Van Strijp JNG;
XX
XX WPI; 2003-256333/25.
XX
XX
XX Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases.
XX
XX Disclosure; Page 17; 89pp; English.
XX

XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
CC Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the C5a-
CC receptor (CSAR) and/or formylated peptide receptor (PPR) or neutrophils,
CC monocytes and endothelial cells or involving acute or chronic
CC inflammation reactions. The diseases or disorders include cardiovascular
CC diseases, disease of the central nervous system, gastrointestinal
CC diseases, skin diseases, genitourinary diseases, joint diseases,
CC respiratory diseases and HIV infection
XX
XX Sequence 6 AA;

Query Match 50.0%; Score 30; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 FFSFLM 9
DB 1 FFSFLM 6

RESULT 5
AAW72493
ID AAW72493 standard; peptide; 9 AA.
XX
AC AAW72493;
XX

DT 23-DEC-1998 (first entry)
XX

DE Dengue virus type-2 glycoprotein NS1 peptide for epitope mapping #38.
XX

XX Dengue virus type-2 glycoprotein NS1; dengue haemorrhagic fever; DHF;
XX dengue shock syndrome; DSS; Aedes aegypti; mosquito; antigen; vaccine;
XX immunisation; immunoreactive; infection.
XX

OS Dengue virus.
XX

XX US5824506-A.
XX

XX 20-OCT-1998.
XX

XX 15-AUG-1994; 94US-00290268.
XX

XX 15-AUG-1994; 94US-00290268.
XX

XX (GENE-) GENELABS DIAGNOSTICS PTE LTD.
XX

XX Chan L, Guan M;
XX

XX WPI; 1998-582552/49.
XX

XX Dengue virus peptide antigens - especially for diagnosis of dengue virus
PT infection.
XX
XX Example 1; Col 17; 21pp; English.
XX

XX AAW72456 to AAW72570 represent peptide fragments from the dengue virus
CC type-2 glycoprotein NS1, which was used in an example from the present

CC invention for an epitope mapping assay. The invention has developed
CC peptide antigens consisting of fragments of the dengue virus NS1 protein.
CC The peptide antigens can be used for the diagnosis of dengue virus
CC infection by detection of antibodies to the virus, especially in an assay
CC comprising attaching the antigen to a solid support, contacting a serum
CC sample with the support, and detecting bound antibodies with a labelled
CC anti-human antibody or used for preparing vaccines against dengue virus
CC infection
XX
SQ Sequence 9 AA;

Query Match 50.0%; Score 30; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 GSFPSELM 9
DB 1 GVFFPTNIM 8

RESULT 6
AAW37198 standard; peptide; 10 AA.
XX
XX AAW37198;
XX
XX 20-JUL-1998 (first entry)
XX
DE Human oncogenic protein MDM2 binding Cys (Acrid) peptide derivative 2.
XX
XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
XX tumour; diagnosis; binding; viral infection.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl; Sulphydryl side-chain linked
FT to 6-acryloyl-2-(dimethylamino) naphthalene"
FT Modified-site 10
FT /note= "C-terminal amide"
XX
XX W09801467-A2.
XX
XX 15-JAN-1998.
XX
XX 04-JUL-1997; 97WO-EP003549.
XX
XX 05-JUL-1996; 96GB-00014197.
XX 07-APR-1997; 97GB-00007041.
XX
XX (NOVS) NOVARTIS AG.
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX Lane D, Boettger V, Boettger A, Pickelley S, Hochkeppel H;
XX Garcia-Echeverria C, Chene P, Furet P;
XX
XX WPI; 1998-100996/09.
XX
XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -
XX useful in, e.g. diagnosis and treatment of cancer and viral infections
XX and identifying binding agents.
XX
XX Example 2; Page 20; 45pp; English.
XX
XX This is a Cys (Acrid) peptide derivative capable of binding to a human
XX oncogenic protein MDM2. The MDM2 binding peptides can specifically
XX inhibit or block the binding of MDM2 to the human p53 protein, in vitro
XX or in vivo. Inhibiting the interaction between the p53 and MDM2 can
XX induce growth arrest or apoptosis in tumour cells comprising a wild-type
XX p53 and non-elevated levels of MDM2. The peptides may be used to identify
XX molecules that bind to MDM2 and to identify and design inhibitors of

CC MDM2/p53 binding. They may also be used to purify binding partners
CC especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
CC cancer and leukaemia patients and for treatment or prevention of disease
CC involving p53/MDM2 interactions, especially tumours and viral infections.
CC The peptides can be administered nasally, rectally, orally or by
CC injection. By interfering with MDM2/p53 interaction, the peptides can
CC activate p53 function and accumulation in normal cells. The peptides
CC which mimic the MDM2 binding site in p53, have a significantly greater
CC blocking activity compared with wild-type p53
XX
SQ Sequence 10 AA;

Query Match 50.0%; Score 30; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 GSFPSELM 9
DB 2 GPRFSDLM 9

RESULT 7
AAW33139 standard; peptide; 7 AA.
XX
XX AAW33139;
XX
XX 16-NOV-1999 (first entry)
XX
XX Rabbit carboxylesterase protein fragment #3.
XX
XX Carboxylesterase; rabbit; tumour cell; chemotherapy; prodrug;
XX disease-specific responsive promoter; CRT-11; APC; resection; recurrence;
XX inhibition; bone marrow cell.
XX
XX Oryctolagus cuniculus.
XX
XX W09942593-A1.
XX
XX 26-AUG-1999.
XX
XX 12-FEB-1999; 99WO-US003171.
XX
XX 19-FEB-1998; 98US-0075258P.
XX
XX (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
XX Danks MK, Potter PM, Houghton PJ;
XX
XX WPI; 1999-540311/45.
XX
XX New carboxylesterase polypeptide for treatment of tumors.
XX
XX Example 2; Page 57; 70pp; English.
XX
XX This invention describes a novel rabbit carboxylesterase polypeptide (I)
XX capable of metabolizing a chemotherapeutic prodrug and its inactive
XX metabolites into an active drug. The invention also describes a
XX composition comprising (I) and a disease-specific responsive promoter.
XX This composition is useful for sensitizing tumor cells to a
XX chemotherapeutic prodrug (preferably CRT-11 or APC) by transfecting into
XX tumor cells, and contacting the sensitized cells with a chemotherapeutic
XX prodrug to inhibit growth of the tumor cells. The composition can also be
XX administered to the site of tumor resection to inhibit tumor recurrence,
XX and be administered to bone marrow cells to remove tumor cells. The
XX products of the invention are useful for identifying drugs that are
XX inactivated by a carboxylesterase enzyme, and are also useful for
XX identifying compounds containing a COOC ester linkage that are activated
XX by a carboxylesterase enzyme. This sequence represents a fragment of a
XX rabbit carboxylesterase which is described in the method of the invention
XX
SQ Sequence 7 AA;

Query Match 48.3%; Score 29; DB 2; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 SPFSSELM 9
: : : : :
1 AFMTSLM 7

RESULT 8
AAU93215
ID AAU93215 standard; peptide; 10 AA.

AC AAU93215;

DT 02-JUL-2002 (first entry)

DE Granulocyte-colony stimulating factor receptor binding peptide #21.

KM G-CSFR; granulocyte-colony stimulating factor receptor; cytokine;

KM haematopoietic growth factor; neutrophil proliferation; AIDS;

KM neutrophil differentiation; acquired immunodeficiency syndrome;

KM chemotherapy-induced neutropenia; community acquired pneumonia;

KM depressed neutrophil count; immunostimulant.

XX Synthetic.

XX WO200207676-A2.

PD 31-JAN-2002.

PF 20-JUL-2001; 2001WO-US023046.

PR 20-JUL-2000; 2000US-00620091.

XX (GLAXO) GLAXO GROUP LTD.

PI Cutila SE, Balu P, Duffin DJ, Piplani S, McEwen-Merrill B;

PI Schatz PJ;

XX WPI; 2002-329382/36.

PT Novel compounds, useful for treating depressed neutrophil count, comprise
peptide chains of approximately 6 to 40 amino acids in length that bind
to granulocyte-colony stimulating factor receptor.

PS Claim 3; Page 52; 90pp; English.

CC The invention relates to compounds comprising a peptide chain

CC approximately 6 to 40 amino acids in length that binds to granulocyte-

CC colony stimulating factor receptor (G-CSFR). The compounds contain

CC specific sequences of the generic peptides appearing as AAU93402-AAU9406

CC and the generic sequences XV 1XV 2XV 3XV 4XV 5XV 6XV 7XV 8 (where XV 1 =

CC E, C, Q, V or Y; XV 2 = E, A, L, M, S, W or Q; XV 3 = X, R or T; XV 4 =

CC L, A or V; XV 5 = R, A, M, H, E, V, L, D, Q or S; XV 6 = E or V; XV 7

CC = A or G; and XV 8 = R, H, G or L) and XVI 1XVI 2XVI 3XVI 4XVI 5

CC EXVI 6XVI 7XVI 8XVI 9 (where XVI 1 = A, E or G; XVI 2 = E, H or D; XVI 3

CC = R or G; XVI 4 = K, Y, M, N, Q, R, D, I, S or E; XVI 5 = A, S or P;

CC XVI 6 = E, D, T, Q, K or A; XVI 7 = R, W, K, L, S, A or Q; XVI 8 = R or B

CC ; and XVI 9 = W, G or R). The compounds are used for treating conditions

CC associated with depressed neutrophil count e.g. chemotherapy- induced

CC neutropenia, AIDS- induced neutropenia or community-acquired pneumonia-

CC induced pneumonia. The compounds are useful as in vitro as tools for

CC understanding the biological role of granulocyte-colony stimulating

CC factor (G-CSF a haematopoietic growth factor) and cytokine that stimulates

CC neutrophil proliferation and differentiation), including evaluation of

CC many factors thought to influence, and be influenced by, production of

CC white blood cells, in the development of compounds that bind to G-CSFR,

CC as reagents for detecting G-CSF receptor or related receptor on living

CC cells, fixed cells, in biological fluid, in tissue homogenates or in

CC purified natural biological materials, in situ staining, fluorescence-

CC activated cell sorting (FACS), Western blotting or enzyme-linked

CC immunoadsorbent assay (ELISA), in receptor purification or in purifying

CC cells expressing G-CSFR on the cell surface (or inside permeabilised
CC cells) as a commercial research reagent for various medical and
CC diagnostic uses or to treat a disease that would benefit from the ability
CC to of a compound to mimic the effects of G-CSF in vivo. The compounds
CC bind specifically to G-CSFR and allow for studies of biological
CC activities mediated by the receptor and for the treatment of diseases,
CC disorders and conditions that would benefit from activating or
CC inactivating G-CSFR. The present sequence is a G-CSFR binding peptide of
CC the invention
CC
XX
SQ Sequence 10 AA;

Query Match 48.3%; Score 29; DB 5; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SPFSSELM 9
: : : : :
3 SFWTELM 9

DB 3 SFWTELM 9

RESULT 9

ABJ37125

ID ABJ37125 standard; peptide; 11 AA.

AC ABJ37125;

DT 08-MAY-2003 (first entry)

DE Rhodopsin related G-protein coupled receptor binding site peptide #1.

KM Compound library; microenvironment; G-protein Coupled Receptor; GPCR;

KM Rhodopsin.

XX Unidentified.

XX WO2003004147-A2.

PD 16-JAN-2003.

PF 05-JUL-2002; 2002WO-GH003094.

PR 06-JUL-2001; 2001GB-00016570.

XX (BIOF-) BIOFOCUS PLC.

PI Crossley R, Rose VS, Stevens AP;

XX WPI; 2003-221549/21.

PT Producing compound library, by generating biological target model using
PT target sequence information, defining microenvironments interacting with
PT ligand and motifs interacting with microenvironment, and assembling
PT motifs.

XX

PS Disclosure; Fig 1; 39pp; English.

XX

CC The invention relates to a novel method for producing a compound library.

CC The novel method involves reducing a biological target into a group of

CC one or more amino acids required for interaction with a ligand, to

CC generate a model of the biological target, using the model to define a

CC microenvironment in the biological target capable of interacting with the

CC ligand, defining motifs which interact with the microenvironment, and

CC assembling the motifs to generate a compound library for synthesis. The

CC natural method is useful to produce compound libraries for screening

CC natural ligands such as peptides and proteins or for producing chemical

CC compounds based on drug motifs for screening. This sequence represents a

CC peptide of a G-protein Coupled Receptor (GPCR) relating to Rhodopsin,

CC which relates to the novel compound library production method of the

XX Sequence 11 AA;

SQ

Query Match 48.3%; Score 29; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ELWTS 11
 |||||
 DB 2 ELWTS 6

RESULT 10

ID ABR46459 standard; peptide: 6 AA.

XX ABR46459;

DT 10-JUN-2003 (first entry)

XX Staphylococcus aureus CHIPS-related peptide #1649.

XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;

KM formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;

KM inflammation; cardiovascular disease; central nervous system disease;

KM gastrointestinal disease; skin disease; genitourinary disease;

KM joint disease; respiratory disease; HIV infection; antiinflammatory;

KM cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;

XX gynecological; immunosuppressive; anti-HIV.

OS Staphylococcus aureus.

XX Synthetic.

XX WO200306048-A1.

XX 23-JAN-2003.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

RESULT 11
 ID ADR68302 standard; peptide: 7 AA.

XX ADR68302;

DT 02-DEC-2004 (first entry)

XX Androgen receptor interacting peptide SEQ ID NO:20.

KM androgen receptor binding peptide; androgen receptor interacting peptide;

KM androgen receptor; cytosolic; gene therapy; prostate cancer.

XX Mammalia.

OS Synthetic.

XX WO2004076473-A2.

XX 10-SEP-2004.

XX 10-FEB-2004; 2004WO-US003774.

XX 12-FEB-2003; 2003US-0446955P.

XX (KARO-) KARO BIO AB.

XX Buehrer BM, Barnett TR;

XX WPI; 2004-653365/63.

XX New polypeptides that bind to the androgen receptor, useful for

PT diagnosing or treating diseases associated with abnormal levels of

PT activation of androgen receptor, e.g. prostate cancer, or in biological

PT research.

XX Disclosure; SEQ ID NO 20; 46pp; English.

XX The present invention describes a polypeptide that binds to the androgen

CC receptor, or a polypeptide that comprises at least 50% amino acid

CC sequence identity to the polypeptide. Also described: (1) methods of

CC analysing the surface conformation of a protein using one or more of the

CC polypeptide sequences mentioned above; (2) methods of identifying

CC modulators of protein function using one or more of the polypeptide

CC sequences mentioned above; (3) a pharmaceutical composition comprising a

CC pharmaceutical carrier and one or more of the polypeptide sequences

CC described above; (4) a peptide that binds to the androgen receptor, the

CC binding being competitively inhibited by the polypeptide described above;

CC (5) a chimeric protein comprising the above polypeptide and at least a

CC portion of a filamentous phage protein, the portion of the filamentous

CC phage protein being sufficient for integration of the chimeric protein

CC into the coat of phage particles to display the polypeptide; (6) a

CC filamentous phage displaying the above polypeptide; (7) a method of

CC diagnosing a disease in a patient characterised by abnormal levels of

CC activation of androgen receptor, comprising providing a sample of body

CC fluid or tissue of the patient, administering a diagnostic amount of the

CC pharmaceutical composition described above, and assaying the amount of

CC activated androgen receptor in the body fluid or tissue of the patient;

CC and (8) a method of treating a patient suffering from a disease

CC characterised by abnormal levels of activation of androgen receptor,

CC comprising administering to the patient a therapeutic amount of the

CC pharmaceutical composition described above. The androgen receptor

CC interacting polypeptide has cytosolic activity, and can be used in gene

CC therapy. The composition and methods are useful for diagnosing or

CC treating patients suffering from diseases characterised by abnormal

CC levels of activation of androgen receptor, such as prostate cancer. They

CC may also be used in biological research, as therapeutics or for in vitro

CC an androgen receptor interacting peptide, which is used in the

CC exemplification of the present invention.

XX Sequence 7 AA;

XX

Query Match 46.7%; Score 28; DB 8; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SFPSSELM 9
| | | | |
| | | | |
Db 1 SRFPAELM 7

RESULT 12

AAV04678
ID AAV04678 standard; peptide; 9 AA.

XX AAV04678;

DT 22-JUN-1999 (first entry)

DE Peptide #13 encoded by HsdR/M/S gene fragment.

KM HsdR; HsdM; HsdS; restriction/modification; bacteriophage; resistance;

XX Lactic acid bacterium.

OS Lactococcus lactis.

PN FR2767831-A1.

PD 05-MAR-1999.

PF 02-SEP-1997; 97FR-00010885.

PR 02-SEP-1997; 97FR-00010885.

PI (INRG) INRA INST NAT RECH AGRONOMIQUE.

DR Chopin MC, Clier F, Ehrlich SD, Gautier M, Schouler C;

XX WPI; 1999-183265/16.

PS Bacteriophage resistance mechanism subunit polypeptides - of lactic acid

XX Bacteria, especially Lactobacillus lactis.

XX Claim 7; Page 62; 65pp; French.

CC The invention relates to polypeptides that constitute the HsdR, HsdM or

CC HsdS subunit of a R/M [restriction/modification] type IC bacteriophage

CC resistance mechanism active against the phages of lactic acid bacteria,

CC especially Lactococcus lactis. Also claimed are fragments of the HsdR,

CC HsdM and HsdS gene which encode peptides AAV04666-Y04679. Nucleic acids

CC encoding the HsdR, HsdM or HsdS fragment can be used for expression of at

CC least one bacteriophage resistance mechanism in a lactic acid bacterium

XX Sequence 9 AA;

QY 2 GSFFSEL 8
| | | | |
| | | | |
Db 2 GSFFKQL 8

RESULT 13

ABB55959
ID ABB55959 standard; peptide; 10 AA.

XX ABB55959;

DT 15-FEB-2002 (first entry)

DE Vascular dementia-associated protein isoform (VPI) 159.

XX Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;

KM diagnosis; prognosis; gene therapy.

XX Homo sapiens.

OS WO200169261-A2.

PN 20-SEP-2001.

PD 14-MAR-2001; 2001WO-GB001106.

PF 15-MAR-2000; 2000GB-00006285.

PR 24-NOV-2000; 2000GB-00028734.

XX 26-NOV-2000; 2000US-00724391.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMA, Parekh RB, Rohlf C;

XX WPI; 2001-557937/62.

PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for

XX determining stage of VD and monitoring the effect of VD therapy,

XX PT comprises analyzing body fluid by 2-dimensional electrophoresis for

XX features correlated with VD.

PS Claim 6; Page 33; 151pp; English.

XX The invention relates to screening, diagnosis or prognosis of Vascular

XX Dementia (VD) in a subject comprising analysing body fluid from the

XX subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of

XX features containing at least one chosen feature whose relative abundance

XX correlates with the presence, absence, stage or severity of VD or

XX predicts the onset or course of VD, especially detecting in a sample of

XX cerebrospinal fluid (CSF) from the subject one of 223 VD-associated

XX protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the

XX specification. Detecting VD-associated features and VPI is useful for the

XX screening, diagnosis or prognosis of VD, for determining the stage or

XX severity of VD, for identifying a subject at risk of VD or for monitoring

XX the effect of therapy administered to a subject having VD. Nucleic acids

XX encoding a VPI or inhibiting the function of a VPI are useful for the

XX treatment of VD and for gene therapy

XX Sequence 10 AA;

QY 3 SFPSSELM 9
| | | | |
| | | | |
Db 1 SFFPENW 7

RESULT 14

AAV93379
ID AAV93379 standard; peptide; 11 AA.

XX AAV93379;

DT 04-SEP-2000 (first entry)

DE Binding moiety for a human parvovirus B19 polypeptide.

XX Binding moiety; human parvovirus; B19 polypeptide; VPI capsid protein;

XX VP2 capsid protein; blood; vaccine.

XX Synthetic.

XX WO200025807-A1.

XX 11-MAY-2000.

XX 04-NOV-1999; 99WO-US026275.

```
XX 05-NOV-1998; 98US-00186958.
XX (DYAX-) DYAX CORP.
XX Whelihan EF;
XX WPI; 2000-365396/31.
XX
XX Human parvovirus B19 polypeptide binding moiety, used to detect, clear
XX and isolate parvovirus B19 polypeptides from blood and other solutions.
XX
XX Claim 2; Page 36; 47pp; English.
XX
XX AAY93377-94 represent binding moieties for human parvovirus B19 or B19-
XX like polypeptides, particularly VP1 or VP2 capsid proteins. AAY93377-85
XX are isolated from a TN7 library, AAY93386-89 are isolated from a TN8
XX library, and AAY93390-94 are isolated from a TN9 library. The B19 binding
XX moieties can be used for detection and clearing of parvovirus B19 and/or
XX B19-like polypeptides from any solution which contains them, e.g. blood.
XX They may also be used to isolate parvovirus B19 and/or B19-like viruses
XX or polypeptides, which may be used in parvovirus vaccines
XX
XX Sequence 11 AA;
SQ
XX
XX Query Match 46.7%; Score 28; DB 3; Length 11;
XX Best Local Similarity 62.5%; Pred. No. 3.6e+02;
XX Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 4 FFSSELMWTS 11
XX 1 FFCALWPS 8
XX
XX Db
XX
XX RESULT 15
XX ADF53467
XX ID ADF53467 standard; peptide; 11 AA.
XX
XX ADF53467;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX MCPC 603 antibody CDR3 mutant peptide amino acid sequence 10.
XX
XX walk-through mutagenesis; prototype amino acid; prototype nucleotide;
XX mutant polypeptide production; MCPC 603;
XX complementarity determining region; CDR; heavy chain; CDR3; mutant;
XX mutein.
XX
XX Unidentified.
XX OS Synthetic.
XX
XX WO2003089671-A1.
XX
XX 30-OCT-2003.
XX
XX 16-APR-2003; 2003WO-US011935.
XX
XX 17-APR-2002; 2002US-0373686P.
XX
XX (CREA/) CREA R.
XX (CAPF/) CAPFUCILLI G.
XX
XX Crea R, Cappuccilli G;
XX
XX WPI; 2003-854132/79.
XX
XX Walk-through mutagenesis of a nucleic acid encoding a polypeptide, useful
XX for producing mutant polypeptides comprising synthesizing oligonucleotides
XX comprising a nucleotide sequence for each target region of a prototype
XX amino acid.
XX
XX Example; Fig 7; 40pp; English.
XX
XX
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```
XX This invention relates to a novel method of walk-through mutagenesis of a
XX nucleic acid encoding a polypeptide which comprises synthesizing a
XX mixture of oligonucleotides comprising a nucleotide sequence for each
XX target region of a prototype amino acid, where each oligonucleotide
XX contains, at each sequence position in the target region, a prototype
XX nucleotide for synthesis of the prototype amino acid, or a predetermined
XX nucleotide that is required for synthesis of the predetermined amino
XX acid. The method is useful in producing mutant polypeptides in which the
XX overall presence of the predetermined amino acid is limited to one or two
XX positions per mutated polypeptide, leaving the remaining amino acids in
XX the targeted region intact or as close as possible to the prototype
XX sequence. The invention was exemplified using the three complementarity
XX determining regions (CDRs) of the heavy chain of the monoclonal antibody
XX MCPC 603.
XX
XX Sequence 11 AA;
SQ
XX
XX Query Match 46.7%; Score 28; DB 7; Length 11;
XX Best Local Similarity 44.4%; Pred. No. 3.6e+02;
XX Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX 3 SFSSELMWTS 11
XX 1 SYSSSSWSS 9
XX
XX Db
XX
XX Search completed: August 3, 2005, 18:38:09
XX Job time : 167 secs
XX
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OM protein - protein search, using sw model

Run on: August 3, 2005, 18:32:08 ; Search time 43 Seconds
(without alignments)
19.096 Million cell updates/sec

Title: US-10-088-681-1
Perfect score: 60
Sequence: 1 TGSFSELMWS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 125705

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	34	56.7	8	4	US-08-468-446-252
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4	34	56.7	8	4	US-08-424-550B-252
5	30	50.0	6	1	US-08-424-957-6
6	30	50.0	6	3	US-09-035-686-6
7	30	50.0	11	1	US-08-424-957-42
8	30	50.0	11	3	US-09-035-686-42
9	29	48.3	7	4	US-09-595-682B-10
10	29	48.3	10	4	US-09-620-091-28
11	28	46.7	11	3	US-09-186-958-6
12	28	46.7	11	3	US-09-669-271A-6
13	28	46.7	11	4	US-09-881-276-6
14	27	45.0	6	1	US-08-277-660A-2
15	27	45.0	6	1	US-08-424-957-2
16	27	45.0	6	3	US-09-035-686-2
17	27	45.0	6	4	US-09-081-975-1
18	27	45.0	6	4	US-09-428-082B-130
19	27	45.0	7	1	US-09-732-384-4
20	27	45.0	7	1	US-08-277-660A-27
21	27	45.0	7	1	US-08-424-957-15
22	27	45.0	7	1	US-08-424-957-19
23	27	45.0	7	3	US-09-035-686-15
24	27	45.0	7	3	US-09-035-686-19
25	27	45.0	10	1	US-08-277-660A-7
26	27	45.0	10	1	US-08-424-957-11
27	27	45.0	10	1	US-08-424-957-18

28	27	45.0	10	3	US-09-035-686-11	Sequence 11, Appl
29	27	45.0	10	3	US-09-035-686-18	Sequence 18, Appl
30	27	45.0	11	1	US-08-277-660A-9	Sequence 9, Appl
31	27	45.0	11	1	US-08-277-660A-10	Sequence 10, Appl
32	27	45.0	11	1	US-08-277-660A-11	Sequence 11, Appl
33	27	45.0	11	1	US-08-277-660A-12	Sequence 12, Appl
34	27	45.0	11	1	US-08-277-660A-13	Sequence 13, Appl
35	27	45.0	11	1	US-08-277-660A-19	Sequence 19, Appl
36	27	45.0	11	1	US-08-277-660A-20	Sequence 20, Appl
37	27	45.0	11	1	US-08-424-957-17	Sequence 17, Appl
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61	25	41.7	11	1	US-08-424-957-44	Sequence 44, Appl
62	25	41.7	11	1	US-08-424-957-45	Sequence 45, Appl
63	25	41.7	11	1	US-08-424-957-46	Sequence 46, Appl
64	25	41.7	11	3	US-09-035-686-4	Sequence 4, Appl
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74	24	40.0	9	4	US-09-971-020A-21	Sequence 21, Appl
75	24	40.0	9	4	US-09-971-020A-22	Sequence 22, Appl
76	24	40.0	9	5	PCT-US94-01258-50	Sequence 50, Appl
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90	23	38.3	6	1	US-08-277-660A-3	Sequence 3, Appl
91	23	38.3	6	1	US-08-424-957-3	Sequence 3, Appl
92	23	38.3	6	1	US-08-424-957-16	Sequence 16, Appl
93	23	38.3	6	3	US-09-035-686-3	Sequence 3, Appl
94	23	38.3	6	3	US-09-035-686-16	Sequence 16, Appl
95	23	38.3	6	4	US-09-081-975-2	Sequence 2, Appl
96	23	38.3	6	4	US-09-732-384-5	Sequence 5, Appl
97	23	38.3	8	4	US-09-402-641-3	Sequence 3, Appl
98	23	38.3	8	4	US-10-339-351-17	Sequence 17, Appl
99	23	38.3	9	4	US-08-403-459-48	Sequence 48, Appl
100	23	38.3	9	4	US-09-402-641-5	Sequence 5, Appl

ALIGNMENTS

```
RESULT 1
US-08-469-260A-252
; Sequence 252, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHRHOF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUTIK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-260A-252

Query Match      56.7%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 FSHLWTS 11
Db      1 FSHLWTS 7

RESULT 2
US-08-488-446-252
; Sequence 252, Application US/08488446
; Patent No. 6558898
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
```

```
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHRHOF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUTIK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-446-252

Query Match      56.7%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 FSHLWTS 11
Db      1 FSHLWTS 7

RESULT 3
US-08-467-344A-252
; Sequence 252, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHRHOF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUTIK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
```


ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,344A
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,550
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 252:
US-08-467-344A-252

Query Match 56.7%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 FSHLWTS 11
Db 1 FSHLWTS 7

RESULT 4
US-08-424-550B-252
Sequence 252, Application US/08424550B
Patent No. 6720166
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MURKHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUTIK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-252

Query Match 56.7%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 FSHLWTS 11
Db 1 FSHLWTS 7

RESULT 5
US-08-424-957-6
Sequence 6, Application US/08424957
Patent No. 570377
GENERAL INFORMATION:
APPLICANT: PICKSLEY, STEVEN M.
APPLICANT: LANE, DAVID P.
TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
TITLE OF INVENTION: Protein and Therapeutic Application Thereof
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Teast, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,957
FILING DATE: 19-APR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/277,660
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-61228/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 398-3249
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-424-957-6

Query Match 50.0%; Score 30; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FSELM 9
Db 2 FSELM 6

RESULT 6

US-09-035-686-6
; Sequence 6, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Picklesley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreyer, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-09-035-686-6

Query Match 50.0%; Score 30; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FSELM 9
Db 2 FSELM 6

RESULT 7
US-08-424-957-42
; Sequence 42, Application US/08424957
; Patent No. 570377
; GENERAL INFORMATION:
; APPLICANT: Picklesley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and p53

; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreyer, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-424-957-42

Query Match 50.0%; Score 30; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FSELM 9
Db 5 FSELM 9

RESULT 8
US-09-035-686-42
; Sequence 42, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Picklesley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/424,957
FILING DATE: 19-APR-1995
APPLICATION NUMBER: US 08/277,660
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-61228/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-09-035-686-42

Query Match 50.0%; Score 30; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 5 SFSELM 9
Db 5 SFSELM 9

RESULT 9
US-09-595-682B-10

Sequence 10, Application US/09595682B
Patent No. 6800483
GENERAL INFORMATION:
APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of
TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-0005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR FILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 7
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-09-595-682B-10

Query Match 48.3%; Score 29; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy 3 SFSELM 9
Db 1 AFWTELM 7

RESULT 10

US-09-620-091-28
Sequence 28, Application US/09620091
Patent No. 6716811
GENERAL INFORMATION:
APPLICANT: CWIRLA, STEVEN E.
APPLICANT: BALU, PALANI
APPLICANT: DUFFIN, DAVID J.
APPLICANT: PIPLANT, SUNILA
APPLICANT: MERRILL, BARBARA MCOWEN

APPLICANT: SCHATZ, PETER JOSEPH
TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
TITLE OF INVENTION: USES
FILE REFERENCE: 0300-0014
CURRENT APPLICATION NUMBER: US/09/620,091
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 491
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-620-091-28

Query Match 48.3%; Score 29; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 3 SFSELM 9
Db 3 SFWTELM 9

RESULT 11
US-09-186-958-6

Sequence 6, Application US/09186958B
Patent No. 6238860
GENERAL INFORMATION:
APPLICANT: Whelihan, E. Fayelle
TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
FILE REFERENCE: Dyax-009.0 US sequence listing
CURRENT APPLICATION NUMBER: US/09/186,958B
CURRENT FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
US-09-186-958-6

Query Match 46.7%; Score 28; DB 3; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 4 FFSELM 11
Db 1 PFCALMPS 8

RESULT 12

US-09-669-271A-6
Sequence 6, Application US/09669271A
Patent No. 6291197
GENERAL INFORMATION:
APPLICANT: Whelihan, E. Fayelle
TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
FILE REFERENCE: Dyax-009.0 US sequence listing
CURRENT APPLICATION NUMBER: US/09/669,271A
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: 09/186,958
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 11

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
US-09-669-271A-6

Query Match 46.7%; Score 28; DB 3; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 FFSLEMTS 11
Db 1 FFCALMPS 8

RESULT 13
US-09-881-276-6
Sequence 6, Application US/09881276
Patent No. 6479641
GENERAL INFORMATION:
APPLICANT: Whelihan, E. Fayelle
TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
FILE REFERENCE: DIX-009.0 US-2
CURRENT APPLICATION NUMBER: US/09/881,276
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 09/669,271
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: 09/186,958
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Microsoft Word 97
SEQ ID NO 6
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polype
US-09-881-276-6

Query Match 46.7%; Score 28; DB 4; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 FFSLEMTS 11
Db 1 FFCALMPS 8

RESULT 14
US-08-277-660A-2
Sequence 2, Application US/08277660A
Patent No. 5702808
GENERAL INFORMATION:
APPLICANT: Picklesley, Steven M.
APPLICANT: Lane, David P.
TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
TITLE OF INVENTION: Protein and Therapeutic Application Thereof
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Teet, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277,660A

FILING DATE: 20-JUL-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Dregler, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-60244/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-277-660A-2

Query Match 45.0%; Score 27; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FSELM 9
Db 2 FSDLM 6

RESULT 15
US-08-424-957-2
Sequence 2, Application US/08424957
Patent No. 5770377
GENERAL INFORMATION:
APPLICANT: Picklesley, Steven M.
APPLICANT: Lane, David P.
TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
TITLE OF INVENTION: Protein and Therapeutic Application Thereof
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Teet, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,957
FILING DATE: 19-APR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/277,660
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dregler, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-61228/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-424-957-2

Query Match 45.0%; Score 27; DB 1; Length 6;

Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSELM 9
||:||||
Db 2 FSDLM 6

Search completed: August 3, 2005, 18:42:34
Job time : 48 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 18:41:15 ; Search time 154 Seconds
(without alignments)
27.829 Million cell updates/sec

Title: US-10-088-681-1

Perfect score: 60

Sequence: 1 TGSFFSLWTS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 227232

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56.7	8	8	US-08-424-5508-252	Sequence 252, App
2	50.0	10	9	US-09-214-371-35	Sequence 35, App1
3	50.0	10	9	US-09-214-371-36	Sequence 36, App1
4	50.0	10	18	US-10-927-262A-35	Sequence 35, App1
5	50.0	10	18	US-10-927-262A-36	Sequence 36, App1
6	48.3	7	16	US-10-858-271-10	Sequence 28, App1
7	48.3	10	17	US-10-659-207-28	Sequence 10, App1
8	46.7	9	9	US-09-486-734A-35	Sequence 35, App1
9	46.7	11	15	US-09-881-276-6	Sequence 6, App1
10	46.7	11	15	US-10-417-895A-56	Sequence 56, App1
11	45.0	6	9	US-09-214-371-83	Sequence 83, App1

12	45.0	27	45.0	6	US-09-732-384-4	Sequence 4, App1
13	45.0	27	45.0	6	US-10-155-059-1	Sequence 1, App1
14	45.0	27	45.0	6	US-10-609-217-130	Sequence 130, App
15	45.0	27	45.0	6	US-10-632-388-130	Sequence 130, App
16	45.0	27	45.0	6	US-10-651-723-130	Sequence 130, App
17	45.0	27	45.0	6	US-10-645-761-130	Sequence 130, App
18	45.0	27	45.0	6	US-10-666-696-130	Sequence 130, App
19	45.0	27	45.0	6	US-10-653-048-130	Sequence 130, App
20	45.0	27	45.0	6	US-10-645-784-130	Sequence 130, App
21	45.0	27	45.0	6	US-10-927-262A-83	Sequence 83, App1
22	45.0	27	45.0	8	US-10-340-179-2	Sequence 2, App1
23	45.0	27	45.0	8	US-10-340-179-3	Sequence 3, App1
24	45.0	27	45.0	9	US-09-214-371-37	Sequence 37, App1
25	45.0	27	45.0	9	US-09-214-371-38	Sequence 38, App1
26	45.0	27	45.0	9	US-10-340-179-1	Sequence 1, App1
27	45.0	27	45.0	9	US-10-927-262A-37	Sequence 37, App1
28	45.0	27	45.0	9	US-10-927-262A-38	Sequence 38, App1
29	45.0	27	45.0	10	US-10-726-332-107	Sequence 107, App
30	45.0	27	45.0	11	US-09-840-085-31	Sequence 31, App1
31	43.3	26	43.3	8	US-10-387-957-36	Sequence 36, App1
32	43.3	26	43.3	8	US-10-387-957-37	Sequence 37, App1
33	43.3	26	43.3	8	US-10-387-957-38	Sequence 38, App1
34	43.3	26	43.3	8	US-10-387-957-39	Sequence 39, App1
35	43.3	26	43.3	8	US-10-387-957-36	Sequence 36, App1
36	43.3	26	43.3	8	US-10-387-957-37	Sequence 37, App1
37	43.3	26	43.3	8	US-10-387-957-38	Sequence 38, App1
38	43.3	26	43.3	8	US-10-387-957-39	Sequence 39, App1
39	43.3	26	43.3	8	US-10-387-955-37	Sequence 37, App1
40	43.3	26	43.3	8	US-10-387-955-38	Sequence 38, App1
41	43.3	26	43.3	8	US-10-387-955-39	Sequence 39, App1
42	43.3	26	43.3	8	US-10-387-955-36	Sequence 36, App1
43	43.3	26	43.3	8	US-10-387-955-37	Sequence 37, App1
44	43.3	26	43.3	8	US-10-387-955-38	Sequence 38, App1
45	43.3	26	43.3	8	US-10-387-955-39	Sequence 39, App1
46	43.3	26	43.3	8	US-10-488-219-37	Sequence 37, App1
47	43.3	26	43.3	8	US-10-488-219-38	Sequence 38, App1
48	43.3	26	43.3	10	US-10-462-452-707	Sequence 707, App
49	43.3	26	43.3	10	US-10-601-953-812	Sequence 812, App
50	43.3	25	43.3	10	US-10-322-266-708	Sequence 708, App
51	41.7	25	41.7	16	US-10-631-722-3	Sequence 3, App1
52	41.7	25	41.7	17	US-10-480-954-233	Sequence 233, App
53	41.7	25	41.7	8	US-10-480-954-235	Sequence 235, App
54	41.7	25	41.7	8	US-10-480-954-237	Sequence 237, App
55	41.7	25	41.7	17	US-10-480-954-239	Sequence 239, App
56	41.7	25	41.7	9	US-10-014-340-245	Sequence 245, App
57	41.7	25	41.7	9	US-10-190-082-180	Sequence 180, App
58	41.7	25	41.7	9	US-10-239-656-11	Sequence 11, App1
59	41.7	25	41.7	17	US-10-893-576-86	Sequence 86, App1
60	41.7	25	41.7	10	US-10-031-874A-14	Sequence 14, App1
61	41.7	25	41.7	10	US-10-611-671-5	Sequence 5, App1
62	41.7	25	41.7	16	US-10-450-036A-14	Sequence 14, App1
63	41.7	25	41.7	10	US-10-327-598-457	Sequence 457, App
64	41.7	25	41.7	10	US-10-725-962-62	Sequence 62, App1
65	41.7	25	41.7	10	US-10-725-962-65	Sequence 65, App1
66	41.7	25	41.7	11	US-10-097-175-60	Sequence 59, App1
67	41.7	25	41.7	11	US-10-417-895A-59	Sequence 59, App1
68	40.8	10	40.8	10	US-10-190-082-167	Sequence 167, App
69	40.8	10	40.8	10	US-10-190-082-170	Sequence 170, App
70	40.8	10	40.8	14	US-10-190-082-171	Sequence 171, App
71	40.8	10	40.8	14	US-10-190-082-290	Sequence 290, App
72	40.0	24	40.0	5	US-10-808-187-581	Sequence 581, App
73	40.0	24	40.0	6	US-10-221-042-3	Sequence 3, App1
74	40.0	24	40.0	9	US-09-086-749A-36	Sequence 36, App1
75	40.0	24	40.0	7	US-09-903-412-36	Sequence 36, App1
76	40.0	24	40.0	7	US-10-174-717A-36	Sequence 36, App1
77	40.0	24	40.0	14	US-10-165-155-36	Sequence 36, App1
78	40.0	24	40.0	7	US-10-197-927-5	Sequence 5, App1
79	40.0	24	40.0	14	US-10-190-162-36	Sequence 36, App1
80	40.0	24	40.0	8	US-10-480-954-51	Sequence 51, App1
81	40.0	24	40.0	8	US-10-480-954-53	Sequence 53, App1
82	40.0	24	40.0	8	US-10-480-954-55	Sequence 55, App1
83	40.0	24	40.0	8	US-10-480-954-119	Sequence 119, App
84	40.0	24	40.0	8	US-10-480-954-121	Sequence 121, App
				17	US-10-480-954-123	Sequence 123, App

85	24	40.0	8	17	US-10-480-954-125	Sequence 125, App
86	24	40.0	8	17	US-10-480-954-151	Sequence 151, App
87	24	40.0	8	17	US-10-480-954-153	Sequence 153, App
88	24	40.0	8	17	US-10-480-954-155	Sequence 155, App
89	24	40.0	8	17	US-10-480-954-157	Sequence 157, App
90	24	40.0	8	17	US-10-480-954-206	Sequence 206, App
91	24	40.0	9	14	US-10-084-813-1011	Sequence 1011, App
92	24	40.0	9	14	US-10-084-813-1012	Sequence 1012, App
93	24	40.0	9	14	US-10-084-813-1013	Sequence 1013, App
94	24	40.0	9	15	US-10-117-937-545	Sequence 545, App
95	24	40.0	9	16	US-10-802-773-19	Sequence 19, App
96	24	40.0	9	16	US-10-802-773-20	Sequence 20, App
97	24	40.0	9	16	US-10-802-773-21	Sequence 21, App
98	24	40.0	9	16	US-10-802-773-22	Sequence 22, App
99	24	40.0	9	16	US-10-657-022-555	Sequence 555, App
100	24	40.0	9	16	US-10-657-022-557	Sequence 557, App

ALIGNMENTS

RESULT 1
US-08-424-550B-252
; Sequence 252, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMM J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAMSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUTIK
; APPLICANT: ISA K. MUSHAMWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/APed
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-424-550B-252

Query Match 56.7%; Score 34; DB 8; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 FSHLWTS 11
Db 1 FSHLWTS 7

RESULT 2
US-09-214-371-35
; Sequence 35, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickstey, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hoeckepel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; NAME/KEY: VARIANT
; LOCATION: (1)
; NAME/KEY: VARIANT
; LOCATION: (10)
; OTHER INFORMATION: X = Pro-NH2
US-09-214-371-35

Query Match 50.0%; Score 30; DB 9; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 GSFRSEW 9
Db 2 GPTFSDW 9

RESULT 3
US-09-214-371-36
; Sequence 36, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickstey, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hoeckepel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 36
; LENGTH: 10

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:peptide
NAME/KEY: VARIANT
LOCATION: (1)
OTHER INFORMATION: X = Ac-Cys
NAME/KEY: VARIANT
LOCATION: (10)
OTHER INFORMATION: x = Pro-NH2
US-09-214-371-36

Query Match 50.0%; Score 30; DB 9; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 GSPFSELM 9
Db 2 GPTFSDLM 9

RESULT 4
US-10-927-262A-35
Sequence 35, Application US/10927262A
Publication No. US20050137137A1
GENERAL INFORMATION:
APPLICANT: LANE, DAVID P
APPLICANT: BOTTER, VOLKER
APPLICANT: BOTTER, ANGELIKA
APPLICANT: PICKSLEY, STEVEN M.
APPLICANT: HOCHKEPPEL, HEINZ-KURT
APPLICANT: GARCIA-ECHEVERRIA, CARLOS
APPLICANT: CHENE, PATRICK
APPLICANT: FURET, PASCAL
TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN P53 AND MDM2
FILE REFERENCE: 39749.0002 APC CON
CURRENT APPLICATION NUMBER: US/10/927,262A
CURRENT FILING DATE: 2004-08-25
PRIOR APPLICATION NUMBER: 09/214,371
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
PRIOR APPLICATION NUMBER: GB 9614197.3
PRIOR FILING DATE: 1996-07-05
PRIOR APPLICATION NUMBER: GB 9707041.1
PRIOR FILING DATE: 1997-04-07
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 35
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Cys(Acrid)
US-10-927-262A-35

Query Match 50.0%; Score 30; DB 18; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 GSPFSELM 9
Db 2 GPTFSDLM 9

RESULT 5
US-10-927-262A-36
Sequence 36; Application US/10927262A

Publication No. US20050137137A1
GENERAL INFORMATION:
APPLICANT: LANE, DAVID P
APPLICANT: BOTTER, VOLKER
APPLICANT: BOTTER, ANGELIKA
APPLICANT: PICKSLEY, STEVEN M.
APPLICANT: HOCHKEPPEL, HEINZ-KURT
APPLICANT: GARCIA-ECHEVERRIA, CARLOS
APPLICANT: CHENE, PATRICK
APPLICANT: FURET, PASCAL
TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN P53 AND MDM2
FILE REFERENCE: 39749.0002 APC CON
CURRENT APPLICATION NUMBER: US/10/927,262A
CURRENT FILING DATE: 2004-08-25
PRIOR APPLICATION NUMBER: 09/214,371
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
PRIOR APPLICATION NUMBER: GB 9614197.3
PRIOR FILING DATE: 1996-07-05
PRIOR APPLICATION NUMBER: GB 9707041.1
PRIOR FILING DATE: 1997-04-07
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 36
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-10-927-262A-36

Query Match 50.0%; Score 30; DB 18; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 GSPFSELM 9
Db 2 GPTFSDLM 9

RESULT 6
US-10-858-271-10
Sequence 10, Application US/10858271
Publication No. US20040259829A1
GENERAL INFORMATION:
APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of
FILE REFERENCE: SJ-0005
CURRENT APPLICATION NUMBER: US/10/858,271
CURRENT FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US/09/595,682
PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR FILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 7
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-10-858-271-10

Query Match 48.3%; Score 29; DB 16; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 SFSELMW 9
:|:|:|
Db 1 AFWTELM 7

RESULT 7

US-10-659-207-28
; Sequence 28, Application US/10659207
; Publication No. US20050037959A1
; GENERAL INFORMATION:
; APPLICANT: CWIRLA, STEVEN E.
; APPLICANT: BALU, PALANI
; APPLICANT: DUFFIN, DAVID J.
; APPLICANT: PIPLANI, SUNILIA
; APPLICANT: MERRILL, BARBARA MCOWEN
; APPLICANT: SCHATZ, PETER JOSEPH
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
; FILE REFERENCE: 0300-0014
; CURRENT APPLICATION NUMBER: US/10/659,207
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US/09/620,091
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-10-659-207-28

Query Match 48.3%; Score 29; DB 17; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 SFSELMW 9
:|:|:|
Db 3 SFWTELM 9

RESULT 8

US-09-486-734A-35
; Sequence 35, Application US/09486734A
; Patent No. US20020164732A1
; GENERAL INFORMATION:
; APPLICANT: Chopin, Marie-Christine
; APPLICANT: Clier, Florence
; APPLICANT: Erlich, S. Dusko
; APPLICANT: Gautier, Michel
; APPLICANT: Schouler, Catherine
; APPLICANT: Institut National de la Recherche Agronomique
; TITLE OF INVENTION: Resistance Mechanisms to Ic Type R/M
; TITLE OF INVENTION: Bacteriophages of Lactic Acid Bacteria
; FILE REFERENCE: 33339/196048
; CURRENT APPLICATION NUMBER: US/09/486,734A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/FR98/01873
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: FR 97/110885
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hsds subunit
; US-09-486-734A-35

Query Match 46.7%; Score 28; DB 9; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GSFFSEL 8
|||:|
Db 2 GSFFKQL 8

RESULT 9

US-09-881-276-6
; Sequence 6, Application US/09881276
; Patent No. US20020031761A1
; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Fayeille
; TITLE OF INVENTION: Binding Molecules for Human Parvovirus B19
; FILE REFERENCE: DYX-009.0 US-2
; CURRENT APPLICATION NUMBER: US/09/881,276
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/669,271
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/186,958
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypep
; US-09-881-276-6

Query Match 46.7%; Score 28; DB 9; Length 11;
Best Local Similarity 62.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 FFCALMPS 11
|||:|
Db 1 FFCALMPS 8

RESULT 10

US-10-417-895A-56
; Sequence 56, Application US/10417895A
; Publication No. US20040033569A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; APPLICANT: Cappuccilli, Guido
; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
; FILE REFERENCE: 1551.2002-001
; CURRENT APPLICATION NUMBER: US/10/417,895A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,686
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variant peptide for third complementarity
; OTHER INFORMATION: determining region of Fv region of an
; OTHER INFORMATION: Immunoglobulin
; US-10-417-895A-56

Query Match 46.7%; Score 28; DB 15; Length 11;
Best Local Similarity 44.4%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 SFSELMWTS 11

Db 1 SYSSSMS 9

```

RESULT 11
US-09-214-371-83
; Sequence 83, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickles, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; TITLE OF INVENTION: Inhibitors of the interaction of p53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 83
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide, amin
US-09-214-371-83

```

Query Match 45.0%; Score 27; DB 9; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.6e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSELM 9
 ||:|
 Db 2 FSDLM 6

```

RESULT 12
US-09-732-384-4
; Sequence 4, Application US/09732384
; Patent No. US20020132977A1
; GENERAL INFORMATION:
; APPLICANT: Yuan, Zhi-Min
; APPLICANT: Gu, Jidie
; TITLE OF INVENTION: Inhibition of p53 Degradation
; FILE REFERENCE: 21508-044
; CURRENT APPLICATION NUMBER: US/09/732,384
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,816
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Protein
; OTHER INFORMATION: Fragment not in inhibitory p53 polypeptide
US-09-732-384-4

```

Query Match 45.0%; Score 27; DB 9; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.6e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSELM 9
 ||:|

Db 2 FSDLM 6

```

RESULT 13
US-10-155-059-1
; Sequence 1, Application US/10155059
; Publication No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THEREFO, AND USES OF THE
; ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESS: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: PastsEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-155-059-1

```

Query Match 45.0%; Score 27; DB 13; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.6e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSELM 9
 ||:|
 Db .2 FSDLM 6

```

RESULT 14
US-10-609-217-130
; Sequence 130, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217

```

```
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-609-217-130
```

```
Query Match          45.0%; Score 27; DB 15; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      5 FSELM 9
        ||:||
Db       2 FSDLM 6
```

```
RESULT 15
US-10-632-388-130
; Sequence 130. Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-632-388-130
```

```
Query Match          45.0%; Score 27; DB 15; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      5 FSELM 9
        ||:||
Db       2 FSDLM 6
```

Search completed: August 3, 2005, 18:54:35
Job time : 162 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 18:50:51 ; Search time 39 Seconds
(without alignments)
29.605 Million cell updates/sec

Title: US-10-088-681-2

Perfect score: 67

Sequence: 1 EYGSFSELMWTS 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Pir 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	30	44.8	10	2	C39191
2	28	41.8	9	2	S36850
3	25	37.3	12	2	PT0274
4	24	35.8	7	2	PH1602
5	22	32.8	9	2	G41946
6	20	29.9	6	2	B34835
7	20	29.9	10	2	T13838
8	20	29.9	11	2	S05002
9	19	28.4	5	2	B61445
10	19	28.4	5	2	A61445
11	19	28.4	6	2	PT0519
12	19	28.4	6	2	A43129
13	19	28.4	7	2	A60224
14	19	28.4	8	2	A41117
15	19	28.4	10	2	A60410
16	19	28.4	11	2	PT0250
17	19	28.4	12	2	I58273
18	18	26.9	9	2	S07241
19	18	26.9	10	2	C41946
20	18	26.9	10	2	S53789
21	18	26.9	11	1	LFTWME
22	18	26.9	11	2	S41747
23	18	26.9	11	2	S33300
24	18	26.9	12	2	S25056
25	18	26.9	12	2	I57678
26	18	26.9	12	2	PH1459
27	17.5	26.1	8	2	JS0315
28	17	25.4	7	2	PT0586
29	17	25.4	8	2	A44960

30	17	25.4	8	2	S08995	hypertrehalosemic
31	17	25.4	8	2	A49823	adipokinetic hormo
32	17	25.4	8	2	A43976	hypertrehalosemic
33	17	25.4	8	2	B43976	hypertrehalosemic
34	17	25.4	8	2	A05169	neuropeptide M-I -
35	17	25.4	10	2	A31571	hypertrehalosemic/
36	17	25.4	11	2	I60434	68kDa neurofilamen
37	17	25.4	12	2	I64829	gene HEXA protein
38	17	25.4	12	2	PH1189	T-cell receptor al
39	17	25.4	12	2	PH1180	T-cell receptor al
40	17	25.4	12	2	PH1183	T-cell receptor al
41	17	25.4	12	2	PH1188	T-cell receptor al
42	17	25.4	12	2	PH1172	T-cell receptor al
43	17	25.4	12	2	PH1175	T-cell receptor al
44	16	23.9	4	2	PT0661	T-cell receptor be
45	16	23.9	7	4	I55382	hypothetical pepti
46	16	23.9	8	2	A32523	peptidyl-dipeptida
47	16	23.9	8	2	S11545	adipokinetic hormo
48	16	23.9	8	2	A61348	red pigment-concen
49	16	23.9	9	2	A28004	adipokinetic hormo
50	16	23.9	8	2	PT0311	Ig heavy chain CRD
51	16	23.9	8	2	A39308	glycine reductase
52	16	23.9	8	2	S11078	glucose-6-phosphat
53	16	23.9	9	2	A24244	adipokinetic hormo
54	16	23.9	9	2	PT0315	Ig heavy chain CRD
55	16	23.9	9	2	A43848	cell surface adhes
56	16	23.9	10	2	S08997	hypertrehalosemic
57	16	23.9	10	2	A60421	hypertrehalosemic
58	16	23.9	10	2	S08998	hypertrehalosemic
59	16	23.9	10	2	A26381	hypertrehalosemic
60	16	23.9	10	2	PT0332	Ig heavy chain CRD
61	16	23.9	10	2	T13976	cytochrome-c oxida
62	16	23.9	10	2	T17057	cytochrome-c oxida
63	16	23.9	10	2	T12303	cytochrome-c oxida
64	16	23.9	10	2	T14019	cytochrome-c oxida
65	16	23.9	10	2	T17060	cytochrome-c oxida
66	16	23.9	10	2	T14043	cytochrome-c oxida
67	16	23.9	10	2	T14054	cytochrome-c oxida
68	16	23.9	10	2	T17066	cytochrome-c oxida
69	16	23.9	10	2	T17069	cytochrome-c oxida
70	16	23.9	10	2	T12308	cytochrome-c oxida
71	16	23.9	10	2	T17072	cytochrome-c oxida
72	16	23.9	10	2	T12312	cytochrome-c oxida
73	16	23.9	10	2	T12316	cytochrome-c oxida
74	16	23.9	10	2	T12321	cytochrome-c oxida
75	16	23.9	10	2	T14219	cytochrome-c oxida
76	16	23.9	11	2	C53652	rhLR protein - pse
77	16	23.9	11	2	PT0302	Ig heavy chain CRD
78	16	23.9	12	2	PH1324	Ig heavy chain DJ
79	16	23.9	12	2	PH1308	Ig heavy chain DJ
80	16	23.9	12	2	S74144	aggrecan - bovine
81	16	23.9	12	2	PH0771	T-cell receptor be
82	16	23.9	12	2	I41235	glutamine-tRNA lig
83	16	23.9	12	2	PH1467	T-cell receptor be
84	16	23.9	12	2	P00776	NADH2 dehydrogenas
85	15	22.4	8	2	S10586	adipokinetic hormo
86	15	22.4	8	2	B27867	homeotic protein U
87	15	22.4	9	2	PT0231	Ig heavy chain CDR
88	15	22.4	10	1	GMROJ2	leucosulfakinin-II
89	15	22.4	10	2	E49033	T-cell receptor ga
90	15	22.4	10	2	F49033	T-cell receptor ga
91	15	22.4	10	2	A40753	aldehyde ferredoxi
92	15	22.4	10	2	B60656	leucosulfakinin II
93	15	22.4	11	1	GMROL	leucosulfakinin II
94	15	22.4	11	1	B49164	chromogranin-B - r
95	15	22.4	11	2	PC2372	58K heat shock pro
96	15	22.4	11	2	P00029	33K protein 3218 -
97	15	22.4	11	2	I52980	glucocerceroidase
98	15	22.4	11	2	A60656	perisulfakinin - A
99	15	22.4	11	2	PC2124	anthocyantrase c
100	15	22.4	12	4	A29169	phospholipase A2 (

ALIGNMENTS

RESULT 1

C39191
hypothetical protein 1 (Terx 5' region) - Bacteroides fragilis
C/Species: Bacteroides fragilis
C/Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 30-Sep-1993
C/Accession: C39191
R/Speer, B.S.; Bedzyk, L.; Salyers, A.A.
J. Bacteriol. 173, 176-183, 1991
A/Title: Evidence that a novel tetracycline resistance gene found on two Bacteroides tra
A/Reference number: A39191; MUID:91100280; PMID:1846135
A/Accession: C39191
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-10 <SPS>
A/Cross-references: GB:M37699

Query Match 44.8%; Score 30; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 FSELWTS 12
: || |||
Db 2 YFSRPWTS 9

RESULT 2

S36850

Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999
C/Accession: S36850
R/Jacob, J.; Kelsoe, G.
Submitted to the EMBL Data Library, July 1992
A/Description: In situ studies on the primary immune response to (4-hydroxy-3-nitropheny
A/Reference number: S25024
A/Accession: S36850
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-9 <UAC>
A/Cross-references: EMBL:X67387; NID:950113; PIDN:CAA47799.1; PID:es1594; PID:g1333871
C/Keywords: heterotetramer; immunoglobulin

Query Match 41.8%; Score 28; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYGSFF 6
: ||| |
Db 4 DYGSYF 9

RESULT 3

PT0274

Ig heavy chain CRD3 region (clone 3-109B) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0274
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A/Reference number: PT0222; MUID:91108337; PMID:1899102
A/Accession: PT0274
A/Molecule type: DNA
A/Residues: 1-12 <YAM>
A/Experimental source: B lymphocyte
C/Keywords: heterotetramer; immunoglobulin

Query Match 37.3%; Score 25; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 FSELWTS 12
: | |||
Db 3 YSSSWTS 9

RESULT 4

PH1602
Ig H chain V-D-J region (wild-type clone 313) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C/Accession: PH1602
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A/Reference number: PH1580; MUID:93301609; PMID:8315387
A/Accession: PH1602
A/Molecule type: DNA
A/Residues: 1-7 <LEV>
A/Experimental source: bone marrow pre-B lymphocyte
C/Keywords: immunoglobulin

Query Match 35.8%; Score 24; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 SELMT 11
: ||| |
Db 3 SSLMT 7

RESULT 5

G41946

T-cell receptor gamma chain (2c.23) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C/Accession: G41946
R/Metsebell, M.; Mosley, R.L.; Whetzel, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A/Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A/Reference number: A41946; MUID:92049316; PMID:1658619
A/Accession: G41946
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-9 <MHS>
C/Keywords: T-cell receptor

Query Match 32.8%; Score 22; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGSFSS 7
: ||| |
Db 2 YGSYSS 7

RESULT 6

B34835

dnaA protein - Pseudomonas aeruginosa (fragment)
C/Species: Pseudomonas aeruginosa
C/Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
C/Accession: B34835
R/Yee, T.W.; Smith, D.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990
A/Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from Bac
A/Reference number: A34835; MUID:90160310; PMID:2106132
A/Accession: B34835
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-6 <YEB>
A/Cross-references: GB:M30125; NID:g151419; PIDN:AAA25916.1; PID:g151421
C/Keywords: DNA binding

Query Match 29.9%; Score 20; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ELW 10
 |||
 Db 4 ELW 6

RESULT 7

T13838

C:Species: cytochrome-c oxidase (EC 1.9.3.1) chain I - Bipes biporus mitochondrion (fragment)

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C/Accession: T13838

R/Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.

A/Title: Two novel gene orders and the role of light-strand replication in rearrangement

A/Reference number: 217789; MUID:97153826; PMID:9000757

A/Accession: T13838

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-10 <MAC>

A/Cross-references: UNIPROT:P92576; EMBL:U71335; NID:G1753232; PID:G1753235; PIDN:AB482

A/Genome: mitochondrion

A/Note: COI

C/Keywords: mitochondrion; oxidoreductase

Query Match 29.9%; Score 20; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SFPS 7
 |||
 Db 6 SFPS 9

RESULT 8

S05002

C:Species: Periplaneta americana (American cockroach)

C/Date: 07-Sep-1990 #sequence_revision 09-Apr-1998 #text_change 09-Jul-2004

C/Accession: S05002

R/Veenstra, J.A.

PEBS Lett. 250, 231-234, 1989

A/Title: Isolation and structure of corazonin, a cardioactive peptide from the american

A/Reference number: S05002; MUID:89325572; PMID:2753132

A/Accession: S05002

A/Molecule type: protein

A/Residues: 1-11 <VEE>

A/Cross-references: UNIPROT:P11496

C/Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/1/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 29.9%; Score 20; DB 2; Length 11;
 Best Local Similarity 42.9%; Pred. No. 2e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FSEWMTS 12
 :|:|:
 Db 5 YSRGWTN 11

RESULT 9

B61445

C:Species: Mytilus edulis (blue mussel)

C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000

C/Accession: B61445

R/Leung, M.K.; Stefano, G.B.

Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984

A/Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis
 A/Reference number: A61445; MUID:84144823; PMID:6583690

A/Accession: B61445

A/Molecule type: protein

A/Residues: 1-5 <LEU>

A/Experimental source: pedal ganglia

C/Keywords: neuropeptide; opioid peptide

Query Match 28.4%; Score 19; DB 2; Length 5;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGSF 5
 |||
 Db 1 YGSF 4

RESULT 10

A61445

C:Species: Mytilus edulis (blue mussel)

C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000

C/Accession: A61445

R/Leung, M.K.; Stefano, G.B.

Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984

A/Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis

A/Reference number: A61445; MUID:84144823; PMID:6583690

A/Accession: A61445

A/Molecule type: protein

A/Residues: 1-5 <LEU>

A/Experimental source: pedal ganglia

C/Keywords: neuropeptide; opioid peptide

Query Match 28.4%; Score 19; DB 2; Length 5;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGSF 5
 |||
 Db 1 YGSF 4

RESULT 11

PT0519

C:Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C/Accession: PT0519

R/Peeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A/Reference number: PT0509; MUID:9127601; PMID:1711558

A/Accession: PT0519

A/Status: translation not shown

A/Molecule type: mRNA

A/Residues: 1-6 <PEE>

A/Experimental source: adult thymus, strain BALB/c

C/Keywords: T-cell receptor

Query Match 28.4%; Score 19; DB 2; Length 6;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 SELW 10
 |||
 Db 2 SELW 5

RESULT 12

A43329

C:Species: Monieza expansa

C/Date: 10-Nov-1997 #sequence_revision 14-Nov-1997 #text_change 09-Jul-2004

C;Accession: A43129
R;MauLe, A.; Shaw, C.; Halton, D.; Thim, L.
Biochem. Biophys. Res. Commun. 193, 1054-1060, 1993
A;Title: GnFfFRamide: A novel FMRFamide-immunoreactive peptide isolated from the sheep
A;Reference number: A43129; MUID:93312289; PMID:8323531
A;Accession: A43129
A;Molecule type: protein
A;Residues: 1-6 <MAU>
A;Cross-references: UNIPROT:P41966
C;Keywords: amidated carboxyl end; neuropeptide
F;6/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 28.4%; Score 19; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 GSFF 6
|||
Db 1 GNFF 4

RESULT 13

A60224
Met-enkephalin-Arg-Phe - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 02-Sep-2000
C;Accession: A60224
R;Madden IV, J.; Evans, C.J.; Tyler, A.N.; Esch, F.S.; Boehlen, P.; Makk, G.; Weber, E.
J. Neurochem. 56, 1914-1920, 1991
A;Title: Isolation and characterization of opioid peptides from rabbit cerebellum.
A;Reference number: A60224; MUID:9125680; PMID:2027006
A;Accession: A60224
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MAD>
C;Superfamily: proenkephalin
C;Keywords: neuropeptide; opioid peptide

Query Match 28.4%; Score 19; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YGSF 5
|||
Db 1 YGSF 4

RESULT 14

A41117
acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)
C;Species: Naja naja oxiana (Asian cobra, Oxa cobra)
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004
C;Accession: A41117
R;Kreienkamp, H.U.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.
Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
A;Title: Anticatalytic sites of the catalytic center of acetylcholinesterase from Torpedo a
A;Reference number: A41117; MUID:91296772; PMID:2068091
A;Accession: A41117
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <KRE>
A;Cross-references: UNIPROT:O7L227
C;Keywords: carboxylic ester hydrolase

Query Match 28.4%; Score 19; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 7 SELW 10
|||
Db 2 AEW 5

RESULT 15

A60410
beta-neoendorphin / dynorphin precursor - guinea pig
N;Alternate names: alpha-neoendorphin; proenkephalin B precursor
C;Species: Cavia porcellus (guinea pig)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 21-Jan-2000
C;Accession: A60410
R;Murphy, R.; Turner, C.A.
Peptides 11, 65-68, 1990
A;Title: Isolation and microsequence analysis of guinea pig alpha-neo-endorphin.
A;Reference number: A60410; MUID:90259864; PMID:2342991
A;Accession: A60410
A;Molecule type: protein
A;Residues: 1-10 <MUR>
C;Superfamily: proenkephalin
C;Keywords: neuropeptide; opioid peptide

Query Match 28.4%; Score 19; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YGSF 5
|||
Db 1 YGSF 4

Search completed: August 3, 2005, 19:00:52
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: August 3, 2005, 18:41:50 ; Search time 165 seconds
(without alignments)
37.242 Million cell updates/sec

Title: US-10-088-681-2
Perfect score: 67
Sequence: 1 EYGSFSELWTS 12

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 4233

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt 03:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	35.8	11	2	077895 oreochromis
2	24	35.8	11	2	077896 oreochromis
3	23	34.3	11	2	P83537 lactobacilli
4	22	32.8	12	2	Q9TR77 bos taurus
5	21	31.3	9	2	O95953 homo sapien
6	20	29.9	10	2	O61A62
7	20	29.9	10	2	P92576
8	20	29.9	11	1	CORZ PERAM
9	20	29.9	11	2	077854
10	20	29.9	11	2	077898
11	20	29.9	11	2	O65CG7
12	20	29.9	12	2	O46664
13	20	29.9	12	2	O61331
14	19	28.4	6	1	FARP MONEX
15	19	28.4	8	2	O99MNO
16	19	28.4	8	2	O7L227
17	19	28.4	10	2	O9TR47
18	19	28.4	10	2	O8SHC6
19	19	28.4	11	2	O9UC46
20	19	28.4	12	2	O53579
21	19	28.4	12	2	O63579
22	18	26.9	8	2	O68LE1
23	18	26.9	8	2	O68LG3
24	18	26.9	9	1	LITR PHYRO
25	18	26.9	9	2	O9HJ33
26	18	26.9	9	2	O8H921
27	18	26.9	9	2	O90350
28	18	26.9	10	1	AKHX_LOCM1
29	18	26.9	10	2	O7M465
30	18	26.9	10	2	O8SHB1
31	18	26.9	10	2	O8SHB4

32	18	26.9	10	2	O8SHB7	O8shb7 furcifer ou
33	18	26.9	10	2	O8SHC0	O8shc0 furcifer la
34	18	26.9	10	2	O8SHC3	O8shc3 furcifer la
35	18	26.9	11	1	LPW_THETH	P05624 thermus the
36	18	26.9	11	1	TKNA_SCYCA	P41333 scyllorhinu
37	18	26.9	11	2	O9UELO	O9uelo homo sapien
38	18	26.9	11	2	O7MIH1	O7mih1 solanum tub
39	18	26.9	12	2	O80Y04	O8oy04 rattus sp.
40	18	26.9	12	2	O89243	O89243 woodchuck h
41	18	26.9	12	2	O8UW00	O8uw00 rana catesb
42	18	26.9	12	2	O90XT0	O90xt0 grus canad
43	18	26.9	12	2	O90XT2	O90xt2 larus glauc
44	18	26.9	12	2	O90XT5	O90xt5 puffinus gr
45	18	26.9	12	2	O90XU4	O90xu4 phalarocor
46	18	26.9	12	2	O12036	O12036 caprine art
47	17.5	26.1	8	1	ICK5_LEUMA	P19987 leucophaea
48	17.5	26.1	11	2	O9G522	O9g522 pseudocalot
49	17	25.4	8	1	HTF1_PERAM	P04548 periplaneta
50	17	25.4	8	1	HTF_TENMO	P67789 tenebrio mo
51	17	25.4	8	1	HTF_ZOPRU	P67790 zophobas ru
52	17	25.4	8	2	O40530	O40530 nicotiana t
53	17	25.4	9	2	O8WGE6	O8wge6 procambatus
54	17	25.4	10	1	HTF_HELZE	P16353 heliothis z
55	17	25.4	10	1	LABA_JATMU	P13270 jatropha mu
56	17	25.4	10	2	O9TUJ3	O9tuj3 canis famli
57	17	25.4	10	2	O7J5U5	O7j5u5 ovis aries
58	17	25.4	11	1	KHBI_KLEBN	P80580 klebsiella
59	17	25.4	11	2	O90735	O90735 gallus gall
60	17	25.4	11	2	O9PS64	O9ps64 gallus gall
61	17	25.4	12	2	O7RFX5	O7rfx5 plasmodium
62	17	25.4	12	2	O70V67	O70v67 prostanther
63	17	25.4	12	2	O70Y72	O70y72 tetradenia
64	16	23.9	5	1	PAP2_PARMA	P81864 pardachirus
65	16	23.9	6	1	E101_LITRU	P82096 litorea rub
66	16	23.9	8	1	AKHG_GRYBI	P67785 gryllus bim
67	16	23.9	8	1	AKH_PROTE	P61856 protophormi
68	16	23.9	8	1	AKH_ROMMI	P67786 romalea mic
69	16	23.9	8	1	RPCN_PANBO	P08939 pandanus bo
70	16	23.9	8	2	O7M3E2	O7m3e2 bos taurus
71	16	23.9	8	2	O94PX5	O94px5 felis silve
72	16	23.9	8	2	O94PX6	O94px6 felis libyc
73	16	23.9	8	2	O94PX7	O94px7 felis silve
74	16	23.9	8	2	O94VA7	O94va7 varanus sal
75	16	23.9	8	2	O94VB2	O94vb2 varanus sal
76	16	23.9	8	2	O94VB5	O94vb5 varanus sal
77	16	23.9	8	2	O70Y57	O70y57 fuerecia af
78	16	23.9	8	2	O7M0L0	O7m0l0 clostridium
79	16	23.9	8	2	O7X145	O7x145 straphylococ
80	16	23.9	8	2	O99NX9	O99nx9 hydrochoeru
81	16	23.9	8	2	O62721	O62721 rattus norv
82	16	23.9	9	1	AKH_HELZE	P67787 heliothis z
83	16	23.9	9	1	O9MW43	O9mw43 homo sapien
84	16	23.9	9	2	O94VC6	O94vc6 varanus pil
85	16	23.9	9	2	O69ID6	O69id6 anolis sagr
86	16	23.9	9	2	O9T688	O9t688 gecko gecko
87	16	23.9	9	2	O38366	O38366 bacterioph
88	16	23.9	9	2	O9RSM1	O9rsm1 staphylococ
89	16	23.9	9	2	O673W5	O673w5 tyrannus me
90	16	23.9	9	2	O673W6	O673w6 terpsiphone
91	16	23.9	9	2	O673W7	O673w7 telophorus
92	16	23.9	9	2	O673W8	O673w8 tchagra ben
93	16	23.9	9	2	O673W9	O673w9 tchagra aus
94	16	23.9	9	2	O673X0	O673x0 rhodophonu
95	16	23.9	9	2	O673X1	O673x1 rhodophonu
96	16	23.9	9	2	O673X2	O673x2 pseudobias
97	16	23.9	9	2	O673X3	O673x3 prionops sc
98	16	23.9	9	2	O673X4	O673x4 prionops re
99	16	23.9	9	2	O673X5	O673x5 platyletra
100	16	23.9	9	2	O673X6	O673x6 otiolus xan

ALIGNMENTS

RESULT 1

077895 PRELIMINARY; PRT; 11 AA.
 AC 077895;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HMC class II B locus 12 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidel;
 OC Cichlidae; Oreochromis.
 RN NCBI_TaxID=8128;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Tillio E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid HMC
 RT class II B loci";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050005; AAC41344.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1367 MW; 3F47C9EA772045A3 CRC64;

Query Match 35.8%; Score 24; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 2.7e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 FFSFLWTS 12
 | : | | | :
 Db 3 FWSILMVA 10

RESULT 2

077896 PRELIMINARY; PRT; 11 AA.
 AC 077896;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HMC class II B locus 12 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidel;
 OC Cichlidae; Oreochromis.
 RN NCBI_TaxID=8128;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Tillio E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid HMC
 RT class II B loci";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050006; AAC41345.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1399 MW; 3F47DB7A772685A3 CRC64;

Query Match 35.8%; Score 24; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 2.7e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 FFSFLW 10
 | : | | | :
 Db 3 FWSILMVA 8

RESULT 3

P83537 PRELIMINARY; PRT; 11 AA.
 AC P83537;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Unknown protein from 2D-page (Fragment).
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 RN NCBI_TaxID=1625;
 RP SEQUENCE, AND INDUCTION.
 RX STRAIN=DSM 20451;
 RX PubMed=12112860;
 RA DOI=10.1002/1615-9861(200206)2:6<765::AID-PROT765>3.0.CO;2-V;
 RA Drews O., Weiss W., Reil G., Parlat H., Walt R., Goerg A.;
 RT "High pressure effects step-wise altered protein expression in
 RT Lactobacillus sanfranciscensis";
 RL Proteomics 2:765-774(2002).
 CC -I- INDUCTION: By elevated hydrostatic pressure.
 CC -I- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
 CC protein is: 65 kDa.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1249 MW; D96C8231B771AD9 CRC64;

Query Match 34.3%; Score 23; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 4.1e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 GSFFS 7
 | | | | :
 Db 1 GSFFA 5

RESULT 4

09TRT7 PRELIMINARY; PRT; 12 AA.
 AC 09TRT7;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE 15 kDa amyloid protein A homolog (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 RN NCBI_TaxID=9913;
 RP SEQUENCE
 RX MEDLINE=92132498; PubMed=1734497;
 RA Velby O.P., Sletten K., Husby G., Nordstoga K.;
 RT "Amino acid sequence analyses of non-AA proteins from amyloid fibrils
 RT of bovine kidney";
 RL Scand. J. Immunol. 35:63-69(1992).
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 12 AA; 1503 MW; 64CDB543C6DBAEB CRC64;

Query Match 32.8%; Score 22; DB 2; Length 12;
 Best Local Similarity 57.1%; Pred. No. 6.6e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 SFFSELM 10
 | | | | :
 Db 1 SFFXEXY 7

RESULT 5

095953 PRELIMINARY; PRT; 9 AA.

AC 095953;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Galactocerobrosidae (EC 3.2.1.46) (Fragment).
 GN Name=GALC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Lull, L., Torchiana E., Finocchiaro G.;
 Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U77631; AAD15626.1; -
 DR GO; GO:0004336; F:galactosylceramidase activity; IEA.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 KM Glycosidase; Hydrolase.
 FT NON_TER
 SQ SEQUENCE 9 AA; 1069 MW; 374E2ADCC2699C8 CRC64;
 Query Match 31.3%; Score 21; DB 2; Length 9;
 Best Local Similarity 37.5%; Pred. No. 1.6e+06;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 3 SPSFSELM 10
 Db 2 GPMVADLM 9
 RESULT 6
 Q6LA62 PRELIMINARY; PRT; 10 AA.
 AC 06LA62;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Amloride-sensitive epithelial sodium channel gamma subunit (Fragment).
 GN Name=SCNN1G;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8642159; PubMed=8824247; DOI=10.1074/jbc.271.42.26062;
 RA Thomas C.P., Doggett N.A., Fisher R., Stokes J.B.;
 RT "Genomic organization and the 5' flanking region of the gamma subunit of the human amloride-sensitive epithelial sodium channel.";
 RL J. Biol. Chem. 271:26062-26066(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86316780; PubMed=8654208;
 RA Ludwig M., Bolkenius U., Wickett L., Marynen P., Bidlingmaier F.;
 RT "Structural organization of the gene encoding the alpha-subunit of the human amloride-sensitive epithelial sodium channel.";
 RL Hum. Genet. 102:576-581(1998).
 DR EMBL; Z92983; CAB07506.1; -
 DR GO; GO:0005216; F:ion channel activity; IEA.
 KM Ionic channel.
 FT NON_TER
 SQ SEQUENCE 10 AA; 1157 MW; DBAF833733B05A2 CRC64;
 Query Match 29.9%; Score 20; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 1.2e+04;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4 SPSFSELM 10
 Db 1 SPSFSELM 10

Db 1 SVVSEKM 7
 RESULT 7
 P92576 PRELIMINARY; PRT; 10 AA.
 AC P92576;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Name=COI;
 OS Bipes biporus (Baja worm lizard).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylia; Squamata; Scleroglossa; Amphisbaenia; Bipedidae; Bipes.
 NC NBI_TaxID=52188;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97153826; PubMed=9000757;
 RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
 RT "Two novel gene orders and the role of light-strand replication in rearrangement of the vertebrate mitochondrial genome.";
 RL Mol. Biol. Evol. 14:91-104(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97153820; PubMed=9000751;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Replication slippage may cause parallel evolution in the secondary structures of mitochondrial transfer RNAs.";
 RL Mol. Biol. Evol. 14:30-39(1997).
 DR EMBL; U71335; AAB48271.1; -
 DR PIR; T13838; T13838.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KM Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 10 AA; 1176 MW; 5B3580C9D5A411A7 CRC64;
 Query Match 29.9%; Score 20; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 SPSF 7
 Db 6 SPSF 9
 RESULT 8
 COR2_PSRM STANDARD; PRT; 11 AA.
 AC P11496;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Corazonin.
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattellidae;
 OC Blattellidae; Periplaneta.
 NC NBI_TaxID=6978;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=89325572; PubMed=2753132; DOI=10.1016/0014-5793(89)80727-6;
 RA Veenstra J.A.;
 RT "Isolation and structure of corazonin, a cardioactive peptide from the American cockroach.";
 RL FEBS Lett. 250:231-234(1989).
 CC -1- FUNCTION: Cardioactive peptide. Corazonin is probably involved in the physiological regulation of the heart beat.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 DR PIR; S05002; S05002.
 KM Amidation; Direct protein sequencing; Neuropeptide;

```
KW Pyrirolidone carboxylic acid.
FT MOD RES 1 1
FT MOD RES 11 11
SQ SEQUENCE 11 AA; 1367 MW; C7CFF32D6415AB46 CRC64;

Query Match
Best Local Similarity 29.9%; Score 20; DB 1; Length 11;
Best Local Similarity 42.9%; Pred. No. 1.3e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FSELMTS 12
DB 5 YSRGWIN 11

RESULT 9
077894 PRELIMINARY; PRT; 11 AA.
AC 077894;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1];
RP SEQUENCE FROM N.A.
RA MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050004; AAC41343.1; -.
FT NON TER 1 1
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;

Query Match
Best Local Similarity 29.9%; Score 20; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 FSELMW 10
DB 3 FMSIWM 8

RESULT 10
077898 PRELIMINARY; PRT; 11 AA.
AC 077898;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1];
RP SEQUENCE FROM N.A.
RA MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050008; AAC41347.1; -.
FT NON TER 1 1
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;
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FT NON TER 1 1
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;

Query Match
Best Local Similarity 29.9%; Score 20; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 FSELMW 10
DB 3 FMSIWM 8

RESULT 11
065CG7 PRELIMINARY; PRT; 11 AA.
AC 065CG7;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Transcriptional activator (Fragment).
GN Name=AC2;
OS Simaria tomato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=71186;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=NI3;
RA Rojas A., Kvarnheden A., Rodriguez D., Valkonen J.P.T.;
RT "A mixture of begomoviruses in severe leaf curl-affected tomatoes in
RT Nicaragua.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ508781; CAD48523.1; -.
FT NON TER 1 1
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1356 MW; 861BC90602D379D5 CRC64;

Query Match
Best Local Similarity 29.9%; Score 20; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SFSELMW 11
DB 4 SFWEVLEPS 11

RESULT 12
046664 PRELIMINARY; PRT; 12 AA.
AC 046664;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Glucose-6-phosphate dehydrogenase (Fragment).
GN Name=G6PD;
OS Macropus robustus robustus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=35580;
RN [1];
RP SEQUENCE FROM N.A.
RA MEDLINE=97224585; PubMed=9060417;
RA Loebe D.A., Johnston P.G.;
RT "Analysis of the intron-exon structure of the G6PD gene of the
RT wallaroo (Macropus robustus) by polymerase chain reaction.";
RL Mamm. Genome 8:146-147(1997).
DR EMBL; U53774; AAC48789.1; -.
FT NON TER 1 1
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1430 MW; D42A9C84E3CB1AA9 CRC64;

Query Match
Best Local Similarity 29.9%; Score 20; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

QY 3 GSFSSE 8
| : |
DB 2 GGYFDE 7

RESULT 13

061331 PRELIMINARY; PRT; 12 AA.
ID 061331;
AC 061331;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE N-acetylglucosamine beta-4 galactosyl transferase (EC 2.4.1.90)
DS (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8903397; PubMed=3141392;
RA Nakazawa K., Ando T., Kimura T., Narimatsu H.;
RT "Cloning and sequencing of a full-length cDNA of mouse N-
acetylglucosamine (beta 1-4)galactosyltransferase.";
RL J. Biochem. 104:165-168(1988).
DR EMBL; D00315; BAA00217.1; -;
DR GO; GO:0003945; F:N-acetylglucosamine synthase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
KM Glycosyltransferase; Transferase.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1283 MW; 304EA40668387728 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 WTS 12
| : |
DB 1 WTS 3

RESULT 14
FARP_MONEX STANDARD; PRT; 6 AA.
ID FARP_MONEX
AC P41966;
DT 01-NOV-1995 (Rel. 32, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE FMRFamide-like neuropeptide GNFPRF-amide.
OS Moniezia expansa (Sheep tapeworm).
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Anoplocephalidae; Moniezia.
OX NCBI_TaxId=28841;
RN [1]
RP SEQUENCE.
RX MEDLINE=93312289; PubMed=8323531;
RA Maule A.G., Shaw C., Halton D.W., Thim L.;
RT "GNFPRFamide: a novel FMRFamide-immunoreactive peptide isolated from
the sheep tapeworm, Moniezia expansa.";
Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
family.
CC PIR: A43129; A43129.
KM Amidation: Direct protein sequencing; Neuropeptide.
MOD_RES 6 Phenylalanine amide.
FT MOD_RES 6 AA; 787 MW; 69D409C9C4481000 CRC64;
SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;

Query Match 28.4%; Score 19; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSFP 6
| : |
DB 1 GNFP 4

RESULT 15

099MNO PRELIMINARY; PRT; 8 AA.
ID 099MNO
AC 099MNO;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Adenosine deaminase tRNA-specific 1 (Fragment).
DS Name=Adact1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SvJ;
RC MEDLINE=2123131; PubMed=11331948;
RA Maas S., Kim Y.G., Rich A.;
RT "Genomic clustering of tRNA-specific adenosine deaminase ADAT1 and two
tRNA synthetases.";
RL Mamm. Genome 12:387-393(2001).
DR EMBL; AF328904; AAK19310.1; -;
DR MGD; MGI:1353631; Adact1.
FT NON_TER 8
SQ SEQUENCE 8 AA; 936 MW; FAD0581ADCB376 CRC64;

Query Match 28.4%; Score 19; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 LMTS 12
| : |
DB 1 MMTA 4

Search completed: August 3, 2005, 18:57:22
Job time : 166 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model1

Run on: August 3, 2005, 18:42:40 ; Search time 159 Seconds
(without alignments)
29.189 Million cell updates/sec

Title: US-10-088-681-2

Perfect score: 67

Sequence: 1 EYGSFSELMWTS 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 520583

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp2000s:*
3: geneseqp2001s:*
4: geneseqp2002s:*
5: geneseqp2003as:*
6: geneseqp2003bs:*
7: geneseqp2003cs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	55	82.1	12 4 AAB86005	Aab86005 DCM-aseoc
2	34	50.7	6 4 AAB97294	Aab97294 Betal-adr
3	34	50.7	6 5 AAM47222	Aam47222 Dilated c
4	34	50.7	6 5 ADP49242	Adp49242 Disease-a
5	34	50.7	8 3 AAB09130	Aab09130 Hepaticis
6	31	46.3	10 8 ADK09671	Adk09671 Human pap
7	31	46.3	10 8 ADK09188	Adk09188 Human pap
8	30	44.8	6 6 ABR46515	Abt46515 Staphyloc
9	30	44.8	9 2 AAW72493	Aaw72493 Dengue vi
10	30	44.8	10 2 AAW76040	Aaw76040 LM609 gra
11	30	44.8	10 2 AAW37198	Aaw37198 Human onc
12	30	44.8	10 4 AAB61398	Aab61398 Multiple
13	30	44.8	10 6 ABO19836	Abol19836 Enhanced
14	30	44.8	10 7 ADG71874	Adg71874 Enhanced
15	30	44.8	10 8 ADU58055	Adu58055 Murine LM
16	29	43.3	7 2 AAY33139	Aay33139 Rabbit ca
17	29	43.3	10 5 AAU93215	Aau93215 Granulocy
18	29	43.3	11 6 ABJ37125	Abj37125 Rhodopsin
19	29	43.3	12 4 AAM00568	Aam00568 Human str
20	28	41.8	6 6 ABR46459	Abt46459 Staphyloc
21	28	41.8	7 8 ADR68302	Adr68302 Androgen
22	28	41.8	8 8 ADK09492	Adk09492 Human pap
23	28	41.8	9 2 AAY04678	Aay04678 Peptide #
24	28	41.8	9 8 ADK09532	Adk09532 Human pap
25	28	41.8	9 8 ADK09531	Adk09531 Human pap

26	28	41.8	9 8 ADK09533	Adk09533 Human pap
27	28	41.8	10 4 ABB55959	Abb55959 Vascular
28	28	41.8	10 8 ADK09606	Adk09606 Human pap
29	28	41.8	11 3 AAY93379	Aay93379 Binding m
30	28	41.8	11 7 ADF53467	Adf53467 MCP6 603
31	27.5	41.0	9 2 AAR58533	Aar58533 Light cha
32	27.5	41.0	9 2 AAR95306	Aar95306 Light cha
33	27	40.3	6 2 AAR89913	Aar89913 p53/MDM2
34	27	40.3	6 2 AAM13606	Aam13606 p53 prote
35	27	40.3	6 3 AAB17074	Aab17074 Mdm/hdm a
36	27	40.3	6 5 ABB73169	Abb73169 Mdm/hdm a
37	27	40.3	6 6 ABR46627	Abt46627 Staphyloc
38	27	40.3	6 6 ABR46507	Abt46507 Staphyloc
39	27	40.3	6 6 ABG73432	Abg73432 Human p53
40	27	40.3	6 7 ADJ73323	Adj73323 Mdm/hdm a
41	27	40.3	6 8 ADJ52957	Adj52957 CH1 delet
42	27	40.3	6 8 ADJ51918	Adj51918 CH1 delet
43	27	40.3	7 2 AAR89921	Aar89921 Antibody
44	27	40.3	7 2 AAR89925	Aar89925 p53 bindi
45	27	40.3	7 3 AAY57789	Aay57789 TRAM-inte
46	27	40.3	8 8 ADQ28799	Adq28799 Human cel
47	27	40.3	8 8 ADQ28800	Adq28800 Human cel
48	27	40.3	8 2 AAW37199	Aaw37199 Human onc
49	27	40.3	9 5 AAE31317	Aae31317 Human p53
50	27	40.3	9 5 AAE31316	Aae31316 Human p53
51	27	40.3	9 5 AAE31395	Aae31395 Human p53
52	27	40.3	9 8 ADK09130	Adk09130 Human pap
53	27	40.3	9 8 ADK09595	Adk09595 Human pap
54	27	40.3	9 8 ADQ28798	Adq28798 Human cel
55	27	40.3	9 8 ADP80098	Adp80098 Human HLA
56	27	40.3	10 2 AAR89917	Aar89917 Human p53
57	27	40.3	10 2 AAM13605	Aam13605 p53 prote
58	27	40.3	10 8 ADG78885	Adg78885 Human p53
59	27	40.3	10 8 ADN48959	Adn48959 Peptide #
60	27	40.3	10 8 ADN64792	Adn64792 HLA bindi
61	27	40.3	10 8 ADP47192	Adp47192 Human pho
62	27	40.3	10 8 ADQ90923	Adq90923 Pancreati
63	27	40.3	10 8 ADP80344	Adp80344 Human HLA
64	27	40.3	10 8 ADT02867	Adt02867 Human p53
65	27	40.3	11 2 AAW11231	Aaw11231 Peptide A
66	27	40.3	11 4 AAU27152	Aau27152 Human Leu
67	27	40.3	11 4 AAU26842	Aau26842 Human Leu
68	27	40.3	11 5 AAM52269	Aam52269 Miniature
69	27	40.3	11 8 ADN64806	Adn64806 HLA bindi
70	27	40.3	11 8 ADP80368	Adp80368 Human HLA
71	27	40.3	12 2 AAR86110	Aar86110 Anti-ELAM
72	27	40.3	12 2 AAW26888	Aaw26888 ELAM-1 bi
73	27	40.3	12 2 AAM63920	Aam63920 ELAM-1 pe
74	27	40.3	12 2 AAW37181	Aaw37181 Human p53
75	27	40.3	12 2 AAW37188	Aaw37188 Human onc
76	27	40.3	12 2 AAW37189	Aaw37189 Human onc
77	27	40.3	12 3 AAB17076	Aab17076 Mdm/hdm a
78	27	40.3	12 3 AAB17087	Aab17087 Mdm/hdm a
79	27	40.3	12 3 AAB17088	Aab17088 Mdm/hdm a
80	27	40.3	12 3 AAB17075	Aab17075 Mdm/hdm a
81	27	40.3	12 3 AAB73170	Abb73170 Mdm/hdm a
82	27	40.3	12 5 ABB73183	Abb73183 Mdm/hdm a
83	27	40.3	12 5 ABB73171	Abb73171 Mdm/hdm a
84	27	40.3	12 5 ABB73182	Abb73182 Mdm/hdm a
85	27	40.3	12 7 ADJ73324	Adj73324 Mdm/hdm a
86	27	40.3	12 7 ADJ73336	Adj73336 Mdm/hdm a
87	27	40.3	12 7 ADJ73337	Adj73337 Mdm/hdm a
88	27	40.3	12 7 ADJ73325	Adj73325 Mdm/hdm a
89	27	40.3	12 8 ADJ34264	Adj34264 Wild type
90	27	40.3	12 8 ADJ52959	Adj52959 CH1 delet
91	27	40.3	12 8 ADJ52971	Adj52971 CH1 delet
92	27	40.3	12 8 ADJ52970	Adj52970 CH1 delet
93	27	40.3	12 8 ADJ52958	Adj52958 CH1 delet
94	27	40.3	12 8 ADJ51920	Adj51920 CH1 delet
95	27	40.3	12 8 ADJ51932	Adj51932 CH1 delet
96	27	40.3	12 8 ADJ51931	Adj51931 CH1 delet
97	27	40.3	12 8 ADJ51919	Adj51919 CH1 delet
98	26	38.8	5 2 AAR25372	Aar25372 Peptide #

99 26 38.8 5 2 AAR89912 AAR89912 p53/MDM2
100 26 38.8 5 2 AAM52022 AAM52022 Peptide #

ALIGNMENTS

RESULT 1

AAB86005
ID AAB86005 standard; peptide; 12 AA.

XX AAB86005;

DT 12-JUL-2001 (first entry)

XX DCM-associated peptide #5.

DE DCM; dilatative cardiomyopathy; autoantibody; cardiast;

KM beta-1 adrenergic activated antibody; immunosuppressive.

XX Synthetic.

OS WO200121660-A1.

XX 29-MAR-2001.

PF 21-SEP-2000; 2000WO-EP009241.

XX 21-SEP-1999; 99EP-00118630.

PR 21-SEP-1999; 99EP-00118631.

XX (AFFI-) AFFINA IMMUNOTECHNIK GMBH.

PI Roenpeck W, Kunze R, Wallukat G, Dierenfeld M;

DR WPI; 2001-335469/35.

PT New peptide useful for combating the autoantibodies that are responsible

XX for dilatative cardiomyopathy.

PS Claim 3; Page 20; 29pp; German.

XX This invention describes a novel peptide (P1) which can be used for (1)

CC isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid

CC phase; and (2) a chromatographic apparatus with (P1) bound. The products

CC of the invention have cardiast and immunosuppressive activity. (P1) is

CC used to produce medicine to combat beta_1 adrenergic activated

CC autoantibodies having a causal pathological relationship with dilatative

CC cardiomyopathy. This sequence represents a specifically claimed peptide

XX used to illustrate the method of the invention

XX Sequence 12 AA;

SO Query Match 82.1%; Score 55; DB 4; Length 12;

ID AAB97294 standard; peptide; 6 AA.

XX AAB97294;

DT 13-AUG-2001 (first entry)

DE Beta1-adrenoceptor secondary loop epitope peptide #3.

XX B cell; toxin; antigen specific; antibody mediated disease; virucide;

KM immunosuppressive; antiinflammatory; antiallergic; antidiabetic;
KM thyromimetic; antithyroid; vasorelaxant; cardiast; antitumor;
KM neuroprotective; antirheumatic; antiarthritic; dermatological;
KM ophtalmological; nephrotoxic; allergy; autoimmune disorder;
KM skin diseases; autoimmune endocrinopathy; vasculitic syndrome;
KM cardiovascular disease; immunohaematologic disorder; neurologic disease;
KM gastrointestinal disease; collagen vascular disease; renal diseases;
KM pulmonary disease; infertility disorder; beta1-adrenoceptor;
KM dilated cardiomyopathy.

XX Unidentified.

XX WO200132853-A1.

XX 10-MAY-2001.

PF 12-OCT-2000; 2000WO-US028157.

XX 29-OCT-1999; 99US-0162464P.

XX (BIOM-) INST APPLIED BIOMEDICINE.

PI Chaplin JW;

DR WPI; 2001-316435/33.

PT B cell clonal toxin useful for treating autoimmune disorders such as

PT Grave's disease, myocardial infarction, Crohn's disease, multiple

PT sclerosis, comprises a group that causes toxin to be internalized by B

XX cell.

PS Disclosure; Page 26; 46pp; English.

XX This invention relates to a B cell clonal toxin. The toxin is made from

CC two moieties, the first causes the toxin to be internalised by a B cell,

CC and the second is a biologically acceptable toxin. The invention includes

CC a method for inactivating/killing an antigen specific B cell. A target B

CC cell is contacted with an effective amount of a B cell clonal toxin. The

CC method is useful for selective immunosuppression in conditions

CC characterised by the presence of an unwanted or deleterious immune

CC response, e.g. in the treatment of antigen specific antibody mediated

CC disease conditions. Use of the B cell clonal toxin can result in

CC immunosuppressive; antiinflammatory; antiallergic; virucide; antidiabetic

CC ; thyromimetic; antithyroid; vasorelaxant; cardiast; antitumor;

CC neuroprotective; antirheumatic; antiarthritic; dermatological;

CC ophtalmological; and nephrotoxic activity. The toxin is particularly

CC useful for treating a host suffering from an antigen specific antibody

CC mediated disease condition, where the antigen specific antibody is

CC produced by an antigen-reactive B cell population present in a host. The

CC toxin is useful for treating allergies, viral disease conditions, and

CC autoimmune disorders. Also treated are skin diseases; autoimmune

CC endocrinopathies; vasculitic syndromes; cardiovascular disease;

CC immunohaematologic disorders; gastrointestinal diseases; neurologic

CC diseases; collagen vascular diseases; renal diseases; pulmonary diseases;

CC and infertility disorders. The present sequence represents a beta1-
CC adrenoceptor epitope. An antibody response to this antigen is implicated
CC in dilated cardiomyopathy, a disorder which may be treated using the
XX toxin of the invention
XX Sequence 6 AA;

Query Match 50.7%; Score 34; DB 4; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYGSFP 6

DB 1 EYGSFP 6

RESULT 3

ID AAM47222 standard; peptide; 6 AA.

XX AC AAM47222;
 XX DT 12-FEB-2002 (first entry)
 XX DE Dilated cardiomyopathy absorbents related peptide #2.
 XX KM Dilated cardiomyopathy; absorbent; beta1 adrenoreceptor;
 XX KM M2 muscarine receptor; antibody.
 XX OS Synthetic.
 XX PN WO200176662-A1.
 XX PD 18-OCT-2001.
 XX PF 09-APR-2001; 2001WO-JP003026.
 XX PR 07-APR-2000; 2000JP-00106915.
 XX PA (KANF) KANEKA CORP.
 XX PI Ogino E, Furuyoshi S, Hirai F, Nishimoto T;
 XX DR WPI; 2002-041274/05.
 XX CC Adorbents for dilated cardiomyopathy, comprises an immobilized compound
 PT capable of selectively removing antibodies against approximately bi
 PT adrenoreceptor and/or M2 muscarine receptors in body fluid without
 PT pretreatment.
 XX PS Claim 3; Page 21; 37pp; Japanese.
 XX CC The present invention relates to a method of immobilising an adsorbent
 CC with a compound capable of binding to an antibody against beta1
 CC adrenoreceptor and/or an antibody against M2 muscarine receptor on a
 CC water-insoluble support. The adsorbents, apparatus and method are useful
 CC for treating dilated cardiomyopathy by removing antibodies against beta1
 CC adrenoreceptor and/or M2 muscarine receptor. The present sequence is a
 CC peptide described in the exemplification of the invention
 XX SQ Sequence 6 AA;
 QY Query Match 50.7%; Score 34; DB 5; Length 6;
 DB Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 EYGSFF 6
 1 EYGSFF 6
 DB 1 EYGSFF 6
 RESULT 4
 ADP49242
 ID ADP49242 standard; peptide; 6 AA.
 AC ADP49242;
 XX DT 09-SEP-2004 (first entry)
 XX DE Disease-associated autoantibody detection method peptide #1.
 XX KM cardiant; gynaecological; immunosuppressive; hypotensive; antipsoriatic;
 KM vasotropic; disease-associated autoantibody; antibody;
 KM G protein-coupled receptor.
 XX OS Unidentified.
 XX PN WO2004051280-A2.
 XX PD 17-JUN-2004.
 XX PF 28-NOV-2003; 2003WO-DE003988.

XX PR 29-NOV-2002; 2002DE-01056897.
 XX PR 27-JAN-2003; 2003DE-01003120.
 XX PR 13-JUN-2003; 2003DE-01027066.
 XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 XX PI Malukut G;
 XX DR WPI; 2004-450802/42.
 XX PT Detecting disease-associated autoantibodies against G protein-coupled
 PT receptors, useful for diagnosing e.g. cardiomyopathy, comprises an
 PT enzymatic or color reaction.
 XX PS Claim 12; Page 49; 57pp; German.
 XX CC The present invention relates to a method for detecting disease-
 CC associated autoantibodies (Ab) directed against G protein-coupled
 CC receptors. This comprises treating a body fluid with a denaturing agent,
 CC treating the precipitate formed with a biotin-containing peptide having
 CC the (partial) sequence of a first and/or second loop of a G protein-
 CC coupled receptor, incubating the mixture with a carrier coated by
 CC (strept)avidin, washing the carrier and incubating it with labeled anti-
 CC immunoglobulin G (IgG) antibody subclases, and performing an enzymatic
 CC or colour reaction. The method is used to detect Ab associated with
 CC dilative or Chagas cardiomyopathy, myocarditis, pre-eclampsia, humoral
 CC kidney rejection, malignant, refractory or pulmonary
 CC hypertension, psoriasis and Raynaud's syndrome. The present invention is
 CC a peptide which can be used in the method of the invention.
 XX SQ Sequence 6 AA;
 QY Query Match 50.7%; Score 34; DB 8; Length 6;
 DB Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 EYGSFF 6
 1 EYGSFF 6
 DB 1 EYGSFF 6
 RESULT 5
 AAB09130
 ID AAB09130 standard; protein; 8 AA.
 AC AAB09130;
 XX DT 06-AUG-2003 (revised)
 DT 30-AUG-2000 (first entry)
 XX DE Hepatitis GB virus protein sequence SEQ ID NO:252.
 XX KM Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;
 KM detection; characterisation; hepatitis.
 XX OS Hepatitis GB virus.
 XX PN US6051374-A.
 XX PD 18-APR-2000.
 XX PF 07-JUN-1995; 95US-00488445.
 XX PR 14-FEB-1994; 94US-00196030.
 PR 13-MAY-1994; 94US-00242654.
 PR 29-JUL-1994; 94US-00283314.
 PR 23-NOV-1994; 94US-00344185.
 PR 23-NOV-1994; 94US-00344190.
 PR 30-JAN-1995; 95US-00377557.
 XX PA (ABBO) ABBOTT LAB.

PI Dawson GU, Leary TP, Muerhoff AS, Pilot-Mariae TV, Buljk SV;
PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;
XX WPI; 2000-338307/29.
DR
XX Detecting target hepatitis GB virus nucleic acid in a test sample
PT suspected of containing HGBV comprises reacting the test sample the HGBV
PT polynucleotide probe and detecting the complex that contains target HGBV.
XX
PS Example 9; Col 331-332; 369pp; English.
XX
CC The present invention describe a method for detecting target hepatitis GB
CC virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of
CC containing HGBV. The method involves reacting (T) with a HGBV
CC polynucleotide probe (I) containing 15 contiguous nucleotides, and which
CC selectively hybridises to the HGBV genome or its full complement, and
CC detecting the complex that contains THN, indicating the presence of
CC target HGBV. The method is used for detecting target HGBV nucleic acid in
CC the test sample suspected of containing HGBV and for characterisation of
CC newly ascertained etiological agent of non-A, non-B, non-C, non-D and non
CC -E hepatitis causing agents collectively termed as hepatitis GB virus.
CC AAAS5270 to AAAS5489 and AAB08985 to AAB09480 represent nucleotide and
CC protein sequences used in the exemplification of the present invention.
CC (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 8 AA;
XX
Query Match 50.7%; Score 34; DB 3; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 6 FSEIWTLS 12
|||
1 FSHLWTS 7
XX
RESULT 6
ADK09671
ID ADK09671 standard; peptide; 10 AA.
XX
AC ADK09671;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human papillomavirus peptide #1726.
XX
KW pathogenic virus; alternative reading frame; antigenic determinant;
KW virucide; vaccine; therapeutic agent; infection; HPV.
XX
OS Human papillomavirus.
XX
PN WO2004011650-A2.
XX
PD 05-FEB-2004.
XX
PF 24-JUL-2003; 2003WO-EP008112.
XX
PR 24-JUL-2002; 2002AT-00001124.
PR 11-JUL-2003; 2003EP-00450171.
XX
PA (INTE-) INTERCELL AG.
XX
PI Matner F, Schmidt W, Habel A;
XX
DR WPI; 2004-169243/16.
XX
PT New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.
XX
PS Claim 18; Page 192; 220pp; English.
XX
CC This invention relates to a novel polypeptide encoded by an alternative

CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
CC invention.
XX
SQ Sequence 10 AA;
XX
Query Match 46.3%; Score 31; DB 8; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 4 SFSSEIWT 11
|||||
1 SFSSEIWT 8
XX
Db 1 SFSSEIWT 8
XX
RESULT 7
ADK09188
ID ADK09188 standard; peptide; 10 AA.
XX
AC ADK09188;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human papillomavirus peptide #1243.
XX
KW pathogenic virus; alternative reading frame; antigenic determinant;
KW virucide; vaccine; therapeutic agent; infection; HPV.
XX
OS Human papillomavirus.
XX
PN WO2004011650-A2.
XX
PD 05-FEB-2004.
XX
PF 24-JUL-2003; 2003WO-EP008112.
XX
PR 24-JUL-2002; 2002AT-00001124.
PR 11-JUL-2003; 2003EP-00450171.
XX
PA (INTE-) INTERCELL AG.
XX
PI Matner F, Schmidt W, Habel A;
XX
DR WPI; 2004-169243/16.
XX
PT New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.
XX
PS Claim 18; Page 187; 220pp; English.
XX
CC This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
CC invention.
XX
SQ Sequence 10 AA;
XX
Query Match 46.3%; Score 31; DB 8; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 SFFSELM 11
| | | | |
| | | | |
DB 1 SFFSRTWS 8

RESULT 8
ID ABR46515 standard; peptide; 6 AA.
XX ABR46515;
AC ABR46515;
XX
XX 10-JUN-2003 (first entry)
DT
XX
XX Staphylococcus aureus CHIPS-related peptide #1705.
DE
XX
XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KM formulated peptide receptor; PPR; neutrophil; monocyte; endothelial cell;
KM inflammation; cardiovascular disease; central nervous system disease;
KM gastrointestinal disease; skin disease; genitourinary disease;
KM joint disease; respiratory disease; HIV infection; anti-inflammatory;
KM cardiac; cerebroprotective; neuroprotective; nootropic; dermatological;
KM synecological; immunosuppressive; anti-HIV.
XX
XX Staphylococcus aureus.
OS Synthetic.
OS
XX WO2003006048-A1.
PN
XX 23-JAN-2003.
PD
XX 11-JUL-2001; 2001WO-EP008004.
PF
XX 11-JUL-2001; 2001WO-EP008004.
PR
XX 11-JUL-2001; 2001WO-EP008004.
XX
XX (JARI-) JARI PHARM BV.
PA
XX Van Kessel CPM, Goeseelaar-De Haas CTC, Kruiflitzer JMW;
PI Van Strijp JAG;
XX
XX WPI; 2003-256333/25.
DR
XX

PT Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases.
XX
XX Disclosure; Page 17; 89pp; English.
PS

XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
CC Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the C5a-
CC receptor (C5aR) and/or formulated peptide receptor (PPR) or neutrophils,
CC monocytes and endothelial cells or involving acute or chronic
CC inflammation reactions. The diseases or disorders include cardiovascular
CC diseases, disease of the central nervous system, gastrointestinal
CC diseases, skin diseases, genitourinary diseases, joint diseases,
CC respiratory diseases and HIV infection
XX

XX Sequence 6 AA:

Query Match 44.8%; Score 30; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SFFSELM 10
| | | | |
| | | | |
DB 1 SFFSELM 6

RESULT 9
AAW72493

ID AAW72493 standard; peptide; 9 AA.
XX
XX
XX AAW72493;
AC
XX
XX 23-DEC-1998 (first entry)
DT
XX
XX Dengue virus type-2 glycoprotein NS1 peptide for epitope mapping #38.
DE
XX
XX Dengue virus type-2 glycoprotein NS1; dengue haemorrhagic fever; DHF;
KM dengue shock syndrome; DSS; Aedes aegypti; mosquito; antigen; vaccine;
KM immunisation; immunoreactive; infection.
XX
XX Dengue virus.
OS
XX US5824506-A.
PN
XX 20-OCT-1998.
PD
XX 15-AUG-1994; 94US-00290268.
PF
XX 15-AUG-1994; 94US-00290268.
PR
XX 15-AUG-1994; 94US-00290268.
PA
XX (GENE-) GENELABS DIAGNOSTICS PTE LTD.
XX
XX Chan L, Guan M;
PI
XX WPI; 1998-582552/49.
DR
XX
XX Dengue virus peptide antigens - especially for diagnosis of dengue virus
PT infection.
PT
XX
XX Example 1; Col 17; 21pp; English.
PS
XX
XX AAW72456 to AAW72570 represent peptide fragments from the dengue virus
CC type-2 glycoprotein NS1, which was used in an example from the present
CC invention for an epitope mapping assay. The invention has developed
CC peptide antigens consisting of fragments of the dengue virus NS1 protein.
CC The peptide antigens can be used for the diagnosis of dengue virus
CC infection by detection of antibodies to the virus, especially in an assay
CC comprising attaching the antigen to a solid support, contacting a serum
CC sample with the support, and detecting bound antibodies with a labelled
CC anti-human antibody or used for preparing vaccines against dengue virus
CC infection
XX
XX Sequence 9 AA;

Query Match 44.8%; Score 30; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 SFFSELM 10
| | | | |
| | | | |
DB 1 GVFFPTNW 8

RESULT 10
ID AAW76040 standard; protein; 10 AA.
XX
XX AAW76040;
AC
XX
XX 02-NOV-1998 (first entry)
DT
XX
XX LM609 grafted antibody V-H region CDR3 protein fragment #16.
DE
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KM LM609; inhibitor; integrin-mediated signal transduction; treatment;
KM diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KM neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KM macular degeneration; osteoporosis; primer; V-H region; CDR;
KM complementarity determining region.
XX
XX Mus sp.

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XX  WO9833919-A2.
XX
XX  06-AUG-1998.
XX
XX  30-JAN-1998; 98WO-US001826.
XX
XX  30-JAN-1997; 97US-00791391.
XX
XX  (IXSY-) IXSYS INC.
XX
XX  Huse WD, Glaser SM;
XX
XX  WPI; 1998-437472/37.
XX
XX  N-PSDB; AAV49877.
XX
XX  Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
XX  integrin - and related grafted antibodies based on murine monoclonal
XX  LM609, also related nucleic acid, used to treat, prevent or diagnose
XX  angiogenesis or restenosis.
XX
XX  Claim 62; Page 43; 129pp; English.
XX
XX  AA676007-W76040 are protein fragments of the grafted monoclonal antibody
XX  LM609 heavy and light chain variable region. LM609 and the antibody
XX  vitaxin bind selectively to integrin alphaVbeta3 and can be used to
XX  inhibit binding of alphaVbeta3 to a ligand and thus block integrin-
XX  mediated signal transduction. This is useful in the treatment, prevention
XX  and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis
XX  and restenosis (but also e.g. (non-)immune inflammation, diabetic
XX  retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
XX  arthritis, macular degeneration, osteoporosis etc.). The antibodies
XX  contain non-murine framework regions so are suitable for use in humans.
XX  Enhanced types of LM609 have affinity more than 90 times greater than
XX  that of parent the parent antibody
XX
XX  Sequence 10 AA;
XX
XX  Query Match 44.8%; Score 30; DB 2; Length 10;
XX  Best Local Similarity 83.3%; Pred. No. 2.2e+02;
XX  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 2 YGSFSS 7
XX  |||||
XX  5 YGSFYS 10
XX
XX  RESULT 11
XX  AAW37198
XX  ID AAW37198 standard; peptide; 10 AA.
XX
XX  AAW37198;
XX
XX  20-JUL-1998 (first entry)
XX
XX  Human oncogenic protein MDM2 binding Cys (Acrid) peptide derivative 2.
XX
XX  MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
XX  tumour; diagnosis; binding; viral infection.
XX
XX  Synthetic.
XX
XX  OS Homo sapiens.
XX
XX  Key
XX  Modified-site 1 Location/Qualifiers
XX  /note= "N-terminal acetyl, Sulphydryl side-chain linked
XX  to 6-acryloyl-2-(dimethylamino) naphthalene"
XX
XX  Modified-site 10
XX  /note= "C-terminal amide"
XX
XX  WO9801467-A2.
XX
XX  15-JAN-1998.
XX

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XX  04-JUL-1997; 97WO-EP003549.
XX
XX  05-JUL-1996; 96GB-00014197.
XX
XX  07-APR-1997; 97GB-00007041.
XX
XX  (NOVS ) NOVARTIS AG.
XX
XX  (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX  Lane D, Boettger V, Boettger A, Picklesley S, Hochkeppel H;
XX  Garcia-Echeverria C, Chene F, Furet P;
XX
XX  WPI; 1998-100996/09.
XX
XX  Compounds binding to MDM2 protein and inhibit its interaction with p53 -
XX  useful in, e.g. diagnosis and treatment of cancer and viral infections
XX  and identifying binding agents.
XX
XX  Example 2; Page 20; 45pp; English.
XX
XX  This is a Cys (Acrid) peptide derivative capable of binding to a human
XX  oncogenic protein MDM2. The MDM2 binding peptides can specifically
XX  inhibit or block the binding of MDM2 to the human p53 protein, in vitro
XX  or in vivo. Inhibiting the interaction between the p53 and MDM2 can
XX  induce growth arrest or apoptosis in tumour cells comprising a wild-type
XX  p53 and non-elevated levels of MDM2. The peptides may be used to identify
XX  molecules that bind to MDM2 and to identify and design inhibitors of
XX  MDM2/p53 binding. They may also be used to purify binding partners
XX  especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
XX  cancer and leukemia patients and for treatment or prevention of disease
XX  involving p53/MDM2 interactions, especially tumours and viral infections.
XX  The peptides can be administered nasally, rectally, orally or by
XX  injection. By interfering with MDM2/p53 interaction, the peptides can
XX  activate p53 function and accumulation in normal cells. The peptides
XX  which mimic the MDM2 binding site in p53, have a significantly greater
XX  blocking activity compared with wild-type p53
XX
XX  Sequence 10 AA;
XX
XX  Query Match 44.8%; Score 30; DB 2; Length 10;
XX  Best Local Similarity 62.5%; Pred. No. 2.2e+02;
XX  Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX  QY 3 GSFSESLM 10
XX  |||||
XX  2 GPTFSDLW 9
XX
XX  RESULT 12
XX  AAB61398
XX  ID AAB61398 standard; peptide; 10 AA.
XX
XX  AAB61398;
XX
XX  03-APR-2001 (first entry)
XX
XX  Multiple mutant VH CDR3 #4.
XX
XX  LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
XX  inflammatory; cancer; retina; restenosis; osteoporosis.
XX
XX  Unidentified.
XX
XX  OS Homo sapiens.
XX
XX  WO200079815-A1.
XX
XX  28-DEC-2000.
XX
XX  23-JUN-2000; 2000WO-US017454.
XX
XX  24-JUN-1999; 99US-00339922.
XX
XX  (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX

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PI Huse WD, Wu H;
XX
XX WPI: 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis.
XX
XX Disclosure; Page 43; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
XX CC exhibiting selective binding affinity to alphavbeta 3 integrin or their
XX CC functional fragments. The antibodies or their functional fragments can be
XX CC used in the diagnosis and treatment of alphavbeta 3-mediated diseases
XX CC such as angiogenesis, inflammatory diseases (such as psoriasis and
XX CC chronic articular rheumatism), disorders associated with inappropriate or
XX CC inopportune invasion of vessels (such as diabetic retinopathy,
XX CC neovascular glaucoma and cancer disorders such as tumours and Kaposi's
XX CC sarcoma), retinal diseases (such as macular degeneration), restenosis and
XX CC osteoporosis
XX
XX Sequence 10 AA;
SQ
Query Match 44.8%; Score 30; DB 4; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 YGSFYS 7
Db ||||:|
5 YGSFYS 10
RESULT 13
ABO19836
XX ID ABO19836 standard; peptide; 10 AA.
XX AC ABO19836;
XX DT 28-AUG-2003 (first entry)
XX DE Enhanced LM609 heavy chain variable region CDR3 #15.
XX
XX LM609; antibody; grafted antibody; alpha_vbeta_3; angiogenesis; CDR;
XX KW alpha_vbeta_3-mediated disease; complementarity determining region;
XX KW restenosis.
XX OS
XX Unidentified.
XX PN US2003028009-A1.
XX
XX 06-FEB-2003.
XX
XX 06-JUL-2001; 2001US-00900590.
XX PF
XX 30-JAN-1998; 98US-00016061.
XX PR
XX (IXSY-) IXSYS INC.
XX PA
XX Huse WD;
XX PI
XX WPI: 2003-492042/46.
XX DR N-PSDB; ACD30195.
XX
XX New Vitaxin or LM609 grafted antibody exhibiting selective binding
XX PT affinity to alphavbeta3, useful for treating an alphavbeta3-mediated
XX PT disease e.g., angiogenesis or restenosis.
XX
XX Claim 62, Page 13; 71pp; English.
XX
XX The invention relates to a Vitaxin or LM609 grafted antibody, exhibiting
XX CC selective binding affinity to alpha_vbeta_3. The Vitaxin or LM609 grafted
XX CC antibody is useful for treating an alpha_vbeta_3-mediated disease e.g.

CC angiogenesis or restenosis. The present sequence represents the amino
CC acid sequence of a LM609 complementarity determining region
XX
XX Sequence 10 AA;
SQ
Query Match 44.8%; Score 30; DB 6; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 YGSFYS 7
Db ||||:|
5 YGSFYS 10
RESULT 14
ADG71874
XX ID ADG71874 standard; protein; 10 AA.
XX AC ADG71874;
XX DT 11-MAR-2004 (first entry)
XX
XX Enhanced LM609 grafted antibody VH region CDR3 #15.
XX DE
XX LM609 grafted antibody; high affinity; alphavbeta3;
XX KW complementarity determining region; CDR; inflammatory disorder;
XX KW immune inflammation; non-immune inflammation;
XX KW chronic articular rheumatism; psoriasis; vessel disorder;
XX KW diabetic retinopathy; neovascular glaucoma; capillary proliferation;
XX KW atherosclerotic plaque; cancer disorder; antiinflammatory; antirheumatic;
XX KW dermatological; immunosuppressive; ophthalmological; humanised.
XX
XX Synthetic.
XX OS
XX Homo sapiens.
XX
XX US6596850-B1.
XX PN
XX 22-JUL-2003.
XX PD
XX 30-JAN-1998; 98US-00016061.
XX PF
XX 30-JAN-1998; 98US-00016061.
XX PR
XX 30-JAN-1998; 98US-00016061.
XX
XX (IXSY-) IXSYS INC.
XX PA
XX Huse WD;
XX PI
XX WPI: 2003-842325/78.
XX DR N-PSDB; ADG71873.
XX
XX New high affinity LM609 grafted antibody exhibiting selective binding to
XX PT alphav-beta3, useful for treating inflammatory disorders such as immune
XX PT and non-immune inflammation, chronic articular rheumatism, psoriasis.
XX
XX Claim 6; SEQ ID NO 100; 66pp; English.
XX
XX The present invention relates to a high affinity LM609 grafted antibody
XX CC exhibiting selective binding to alphavbeta3, or its functional fragment
XX CC comprising one or more complementarity determining regions (CDRs) having
XX CC at least one amino acid substitution in one or more CDRs of the LM609
XX CC grafted heavy chain variable region of a polypeptide having 117 amino
XX CC acids or a grafted light chain variable region polypeptide having 107
XX CC amino acids. Also disclosed are polynucleotide sequences encoding the
XX CC novel antibody or its functional fragment, and a composition comprising
XX CC the novel antibody or its functional fragment. The antibodies and their
XX CC fragments are useful for treating alphavbeta3-mediated diseases, e.g.
XX CC inflammatory disorders such as immune and non-immune inflammation,
XX CC chronic articular rheumatism, psoriasis, disorders associated with
XX CC inappropriate or inopportune invasion of vessels such as diabetic
XX CC retinopathy, neovascular glaucoma, and capillary proliferation in
XX CC atherosclerotic plaques as well as cancer disorders. The present sequence
XX CC represents an antibody region.

SQ Sequence 10 AA;

Query March 44.8%; Score 30; DB 7; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGSFYS 7
|||:|
Db 5 YGSFYS 10

RESULT 15

ADJ58055
ID ADJ58055 standard; peptide; 10 AA.

XX ADJ58055;

XX 06-MAY-2004 (first entry)

XX Murine LM609 heavy chain variable region (VH) CDR3 mutant peptide #15.

XX Vitaxin; antibody; LM609; angiogenesis; restenosis; therapy;

XX variable region; mouse; mutant; mutain.

XX Mus SP.

XX Synthetic.

XX US2004006213-A1.

XX 08-JAN-2004.

XX 16-JUN-2003; 2003US-00463847.

XX 30-JAN-1997; 97US-00791391.

XX 30-JAN-1998; 98US-00016061.

XX (IXSY-) IXSYS INC.

XX Huse WD, Glaser SM;

XX WPI; 2004-081749/08.

XX New Vitaxin antibody and a LM609 grafted antibody exhibiting selective

XX binding affinity to alphavbeta3, useful for treating alphavbeta3-mediated

XX diseases, e.g. angiogenesis or restenosis.

XX Claim 62; SEQ ID NO 100; 69pp; English.

XX The present invention provides a Vitaxin antibody and a LM609 grafted

XX antibody exhibiting selective binding affinity to alpha-v-beta-3. The

XX invention is useful for treating alpha-v-beta-3-mediated diseases such as

XX angiogenesis and restenosis. The present sequence is murine LM609

XX antibody variable region CDR mutant peptide.

XX Sequence 10 AA;

Query March 44.8%; Score 30; DB 8; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGSFYS 7
|||:|
Db 5 YGSFYS 10

Search completed: August 3, 2005, 19:00:09
Job time : 162 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OW protein - protein search, using sw model

Run on: August 3, 2005, 18:54:46 ; Search time 42 Seconds
(without alignments)
21.328 Million cell updates/sec

Title: US-10-088-681-2
Perfect score: 67
Sequence: 1 EVGSPFSELTWS 12

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 135920

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	50.7	8	4	US-08-469-260A-252
2	34	50.7	8	4	US-08-488-446-252
3	34	50.7	8	4	US-08-467-344A-252
4	34	50.7	8	4	US-08-424-550B-252
5	30	44.8	6	1	US-08-424-957-6
6	30	44.8	6	3	US-09-035-686-6
7	30	44.8	10	4	US-09-339-922A-100
8	30	44.8	10	4	US-09-016-061-100
9	30	44.8	11	1	US-08-424-957-42
10	30	44.8	11	3	US-09-035-686-42
11	29	43.3	7	4	US-09-595-662B-10
12	29	43.3	10	4	US-09-620-091-28
13	28	41.8	11	3	US-09-186-958-6
14	28	41.8	11	3	US-09-669-271A-6
15	28	41.8	11	4	US-09-881-276-6
16	27.5	41.0	9	1	US-08-300-386A-50
17	27.5	41.0	9	3	US-08-931-645-50
18	27.5	41.0	9	5	PCT-US94-01258-50
19	27.5	41.0	9	5	PCT-US95-11235-50
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21	27	40.3	6	1	US-08-424-957-2
22	27	40.3	6	3	US-09-035-686-2
23	27	40.3	6	4	US-09-081-975-1
24	27	40.3	6	4	US-09-428-082B-130
25	27	40.3	6	4	US-09-732-384-4
26	27	40.3	7	1	US-08-277-660A-27
27	27	40.3	7	1	US-08-424-957-15

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33	27	40.3	10	1	US-08-424-957-18	Sequence 18, Appl
34	27	40.3	10	3	US-09-035-686-11	Sequence 11, Appl
35	27	40.3	10	3	US-09-035-686-18	Sequence 18, Appl
36	27	40.3	11	1	US-08-277-660A-9	Sequence 9, Appl
37	27	40.3	11	1	US-08-277-660A-10	Sequence 10, Appl
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51	27	40.3	11	1	US-08-424-957-36	Sequence 36, Appl
52	27	40.3	11	1	US-08-424-957-43	Sequence 43, Appl
53	27	40.3	11	3	US-09-035-686-17	Sequence 17, Appl
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57	27	40.3	11	3	US-09-035-686-26	Sequence 26, Appl
58	27	40.3	11	3	US-09-035-686-32	Sequence 32, Appl
59	27	40.3	11	3	US-09-035-686-34	Sequence 34, Appl
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63	27	40.3	11	4	US-09-603-052-5	Sequence 5, Appl
64	27	40.3	12	1	US-08-241-054-95	Sequence 95, Appl
65	27	40.3	12	1	US-08-390-156A-45	Sequence 45, Appl
66	27	40.3	12	1	US-08-439-817-75	Sequence 75, Appl
67	27	40.3	12	1	US-08-485-508-95	Sequence 95, Appl
68	27	40.3	12	4	US-09-428-082B-131	Sequence 131, Appl
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71	27	40.3	12	4	US-09-428-082B-144	Sequence 144, Appl
72	27	40.3	5	1	US-07-805-727-13	Sequence 13, Appl
73	26	38.8	5	1	US-08-390-272-13	Sequence 13, Appl
74	26	38.8	5	1	US-08-388-321-13	Sequence 13, Appl
75	26	38.8	5	1	US-08-466-632-13	Sequence 13, Appl
76	26	38.8	5	1	US-08-446-177-13	Sequence 13, Appl
77	26	38.8	5	1	US-08-424-957-5	Sequence 5, Appl
78	26	38.8	5	3	US-09-053-936A-13	Sequence 13, Appl
79	26	38.8	5	3	US-09-035-686-5	Sequence 5, Appl
80	26	38.8	5	3	US-09-490-580-13	Sequence 13, Appl
81	26	38.8	5	3	US-09-442-027-13	Sequence 13, Appl
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83	26	38.8	5	4	US-08-999-188-13	Sequence 13, Appl
84	26	38.8	5	4	US-09-465-126B-12	Sequence 12, Appl
85	26	38.8	5	4	US-09-063-933-13	Sequence 13, Appl
86	26	38.8	6	1	US-07-718-577-8	Sequence 8, Appl
87	26	38.8	6	1	US-07-718-577-9	Sequence 9, Appl
88	26	38.8	7	4	US-09-756-223A-12	Sequence 12, Appl
89	26	38.8	10	1	US-08-321-625-74	Sequence 74, Appl
90	26	38.8	10	3	US-09-161-083-74	Sequence 74, Appl
91	26	38.8	10	4	US-09-339-922A-66	Sequence 66, Appl
92	26	38.8	10	4	US-09-339-922A-98	Sequence 98, Appl
93	26	38.8	10	4	US-09-016-061-66	Sequence 66, Appl
94	26	38.8	10	4	US-09-016-061-98	Sequence 98, Appl
95	26	38.8	10	4	US-09-750-754-74	Sequence 74, Appl
96	26	38.8	12	1	US-08-439-817-200	Sequence 200, Appl
97	25	37.3	6	1	US-07-943-709-13	Sequence 13, Appl
98	25	37.3	6	1	US-07-943-709-16	Sequence 16, Appl
99	25	37.3	6	1	US-07-943-709-24	Sequence 24, Appl
100	25	37.3	10	4	US-09-339-922A-68	Sequence 68, Appl

ALIGNMENTS

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RESULT 1
US-08-469-260A-252
; Sequence 252, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-260A-252

Query Match      50.7%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 FSEIWMTS 12
Db      1 FSHLMTS 7

RESULT 2
US-08-488-446-252
; Sequence 252, Application US/08488446
; Patent No. 6558698
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
```

```
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUERHOF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-446-252

Query Match      50.7%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 FSEIWMTS 12
Db      1 FSHLMTS 7

RESULT 3
US-08-467-344A-252
; Sequence 252, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
```


ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,344A
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,550
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 252:
US-08-467-344A-252

Query Match 50.7%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 4,1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FSHLWTS 12
|||
1 FSHLWTS 7

Db 1 FSHLWTS 7

RESULT 4
US-08-424-550B-252
Sequence 252, Application US/08424550B
Patent No. 6720166
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMT J. PILOT-MATIAS
APPLICANT: GEORGE J. DAMSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MURRHOF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUTIK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-938-2623
TELEFAX: 708-937-6365
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-252

Query Match 50.7%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 4,1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FSHLWTS 12
|||
1 FSHLWTS 7

Db 1 FSHLWTS 7

RESULT 5
US-08-424-957-6
Sequence 6, Application US/08424957
Patent No. 570377
GENERAL INFORMATION:
APPLICANT: PICKLEY, Steven M.
APPLICANT: Lane, David P.
TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
TITLE OF INVENTION: Protein and Therapeutic Application Thereof
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,957
FILING DATE: 19-APR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/277,660
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-61228/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-424-957-6

Query Match 44.8%; Score 30; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FSELM 10
|||
Db 2 FSELM 6

RESULT 6

US-09-035-686-6
; Sequence 6, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Pickelley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,686
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/424,957
FILING DATE: 19-APR-1995
APPLICATION NUMBER: US 08/277,660
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-61228/WHH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown

US-09-035-686-6

Query Match 44.8%; Score 30; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FSELM 10
|||
Db 2 FSELM 6

RESULT 7

US-09-339-922A-100

; Sequence 100, Application US/09339922A
; Patent No. 6531580
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic

; TITLE OF INVENTION: Acids Encoding Same and Methods of Use
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 100
; LENGTH: 10
; TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Mutated
OTHER INFORMATION: complementarity determining region (CDR)
US-09-339-922A-100

Query Match 44.8%; Score 30; DB 4; Length 10;
Best Local Similarity 83.3%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGSFYS 7
|||
Db 5 YGSFYS 10

RESULT 8

US-09-016-061-100
; Sequence 100, Application US/09016061
; Patent No. 6596850

GENERAL INFORMATION:

APPLICANT: Huse, William D.
APPLICANT: Glaeser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-016-061-100

Query Match 44.8%; Score 30; DB 4; Length 10;
Best Local Similarity 83.3%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGSFYS 7

Db 5 YGSFYS 10

RESULT 9

US-08-424-957-42
Sequence 42, Application US/08424957
Patent No. 5770377

GENERAL INFORMATION:

APPLICANT: Pickleley, Steven M.
APPLICANT: Lane, David P.

TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
TITLE OF INVENTION: Protein and Therapeutic Application Thereof

NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Teet, Albilton & Herbert
STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco
STATE: California

COUNTRY: United States
ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,957

FILING DATE: 19-APR-1995
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/277,660

FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-61228/WHD
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249

TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids

TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: unknown
US-08-424-957-42

Query Match 44.8%; Score 30; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 72;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FSELM 10
Db 5 FSELM 9

RESULT 10
US-09-035-686-42

Sequence 42, Application US/09035686
Patent No. 6153391

GENERAL INFORMATION:
APPLICANT: Pickleley, Steven M.

APPLICANT: Lane, David P.
TITLE OF INVENTION: Interruption of Binding of MDM2 and p53

TITLE OF INVENTION: Protein and Therapeutic Application Thereof
NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Teet, Albilton & Herbert

STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco

STATE: California

COUNTRY: United States
ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/277,660

FILING DATE: 19-APR-1995
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/424,957

FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-61228/WHD
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249

TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids

TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: unknown
US-09-035-686-42

Query Match 44.8%; Score 30; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 72;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FSELM 10
Db 5 FSELM 9

RESULT 11
US-09-595-682B-10

Sequence 10, Application US/09595682B
Patent No. 6800483

GENERAL INFORMATION:
APPLICANT: Dankes, Mary K.

APPLICANT: Potter, Philip M.
TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of

TUMOR CELLS
FILE REFERENCE: SJ-0005
CURRENT APPLICATION NUMBER: US/09/595,682B

PRIOR FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258

PRIOR FILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: PCT/US99/03171

PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patent Ver. 2.0
SEQ ID NO 10

LENGTH: 7
TYPE: PRT
ORGANISM: Oryctolagus cuniculus

US-09-595-682B-10
Query Match 43.3%; Score 29; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 SFSELM 10
Db 1 AFWEELM 7

RESULT 12
US-09-620-091-28
; Sequence 28, Application US/09620091
; Patent No. 6716811
; GENERAL INFORMATION:
; APPLICANT: CWIRLA, STEVEN E.
; APPLICANT: BAIU, PALANI
; APPLICANT: DUFFIN, DAVID J.
; APPLICANT: PIPLANI, SUNIL
; APPLICANT: MERRILL, BARBARA MCEOWEN
; APPLICANT: SCHATZ, PETER JOSEPH
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
; TITLE OF INVENTION: USES
; FILE REFERENCE: 0300-0014
; CURRENT APPLICATION NUMBER: US/09/620,091
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-620-091-28

Query Match 43.3%; Score 29; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 97;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 4 SFSELM 10
DB 3 SFVWELM 9
RESULT 13
US-09-186-958-6
; Sequence 6, Application US/09186958B
; Patent No. 6238860
; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Fayelle
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: Dyax-009.0 US sequence listing
; CURRENT APPLICATION NUMBER: US/09/186,958B
; CURRENT FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
; OTHER INFORMATION: binding polypeptide
US-09-186-958-6

Query Match 41.8%; Score 28; DB 3; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 FFSELM 12
DB 1 FFCALMPS 8

RESULT 14
US-09-669-271A-6
; Sequence 6, Application US/09669271A
; Patent No. 6291197

; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Fayelle
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: Dyax-009.0 US sequence listing
; CURRENT APPLICATION NUMBER: US/09/669,271A
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/186,958
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
; OTHER INFORMATION: binding polypeptide
US-09-669-271A-6

Query Match 41.8%; Score 28; DB 3; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 FFSELM 12
DB 1 FFCALMPS 8

RESULT 15
US-09-881-276-6
; Sequence 6, Application US/09881276
; Patent No. 6479641
; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Fayelle
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: DYX-009.0 US-2
; CURRENT APPLICATION NUMBER: US/09/881,276
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/669,271
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/186,958
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypep
US-09-881-276-6

Query Match 41.8%; Score 28; DB 4; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 FFSELM 12
DB 1 FFCALMPS 8

Search completed: August 3, 2005, 19:04:17
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 18:51:56 ; Search time 151 Seconds
(without alignments)
30.962 Million cell updates/sec

Title: US-10-088-681-2

Perfect score: 67

Sequence: 1 EYGSFSELTWS 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 243143

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*
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3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/2/pubppa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubppa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubppa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubppa/US10F_PUBCOMB.pep.*
19: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubppa/US11_PUBCOMB.pep.*
21: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	50.7	6	US-10-221-042-2	Sequence 2, Appl1
2	34	40.7	8	US-08-424-5508-252	Sequence 252, App
3	30	44.8	10	US-09-214-371-35	Sequence 35, Appl
4	30	44.8	10	US-09-214-371-36	Sequence 36, Appl
5	30	44.8	10	US-09-900-590-100	Sequence 100, App
6	30	44.8	10	US-10-305-231-100	Sequence 100, App
7	30	44.8	10	US-10-463-847-100	Sequence 100, App
8	30	44.8	10	US-10-927-262A-35	Sequence 35, Appl
9	30	44.8	10	US-10-927-262A-36	Sequence 36, Appl
10	29	43.3	7	US-10-858-271-10	Sequence 10, Appl
11	29	43.3	10	US-10-659-207-28	Sequence 28, Appl

12	28	41.8	9	US-09-486-734A-35	Sequence 35, Appl
13	28	41.8	11	US-09-881-276-6	Sequence 6, Appl
14	28	41.8	15	US-10-417-895A-56	Sequence 56, Appl
15	27	40.3	6	US-09-214-371-83	Sequence 83, Appl
16	27	40.3	6	US-09-732-384-4	Sequence 4, Appl1
17	27	40.3	6	US-10-155-059-1	Sequence 1, Appl1
18	27	40.3	6	US-10-609-217-130	Sequence 130, App
19	27	40.3	6	US-10-632-388-130	Sequence 130, App
20	27	40.3	6	US-10-651-723-130	Sequence 130, App
21	27	40.3	6	US-10-645-761-130	Sequence 130, App
22	27	40.3	6	US-10-666-696-130	Sequence 130, App
23	27	40.3	6	US-10-653-048-130	Sequence 130, App
24	27	40.3	6	US-10-645-784-130	Sequence 130, App
25	27	40.3	8	US-10-927-262A-83	Sequence 83, Appl
26	27	40.3	8	US-10-340-179-2	Sequence 2, Appl1
27	27	40.3	8	US-10-340-179-3	Sequence 3, Appl1
28	27	40.3	9	US-09-214-371-37	Sequence 37, Appl
29	27	40.3	9	US-09-214-371-38	Sequence 38, Appl
30	27	40.3	9	US-10-340-179-1	Sequence 1, Appl1
31	27	40.3	9	US-10-927-262A-37	Sequence 37, Appl
32	27	40.3	9	US-10-927-262A-38	Sequence 38, Appl
33	27	40.3	10	US-10-726-332-107	Sequence 107, App
34	27	40.3	11	US-09-840-085-31	Sequence 31, Appl
35	27	40.3	12	US-09-214-371-17	Sequence 17, Appl
36	27	40.3	12	US-09-214-371-24	Sequence 24, Appl
37	27	40.3	12	US-09-214-371-25	Sequence 25, Appl
38	27	40.3	12	US-10-609-217-131	Sequence 131, App
39	27	40.3	12	US-10-609-217-132	Sequence 132, App
40	27	40.3	12	US-10-609-217-143	Sequence 143, App
41	27	40.3	12	US-10-609-217-144	Sequence 144, App
42	27	40.3	12	US-10-632-388-131	Sequence 131, App
43	27	40.3	12	US-10-632-388-132	Sequence 132, App
44	27	40.3	12	US-10-632-388-143	Sequence 143, App
45	27	40.3	12	US-10-632-388-144	Sequence 144, App
46	27	40.3	12	US-10-651-723-131	Sequence 131, App
47	27	40.3	12	US-10-651-723-132	Sequence 132, App
48	27	40.3	12	US-10-651-723-143	Sequence 143, App
49	27	40.3	12	US-10-651-723-144	Sequence 144, App
50	27	40.3	12	US-10-645-761-131	Sequence 131, App
51	27	40.3	12	US-10-645-761-132	Sequence 132, App
52	27	40.3	12	US-10-645-761-143	Sequence 143, App
53	27	40.3	12	US-10-645-761-144	Sequence 144, App
54	27	40.3	12	US-10-666-696-131	Sequence 131, App
55	27	40.3	12	US-10-666-696-132	Sequence 132, App
56	27	40.3	12	US-10-666-696-143	Sequence 143, App
57	27	40.3	12	US-10-666-696-144	Sequence 144, App
58	27	40.3	12	US-10-653-048-131	Sequence 131, App
59	27	40.3	12	US-10-653-048-132	Sequence 132, App
60	27	40.3	12	US-10-653-048-143	Sequence 143, App
61	27	40.3	12	US-10-653-048-144	Sequence 144, App
62	27	40.3	12	US-10-645-784-131	Sequence 131, App
63	27	40.3	12	US-10-645-784-132	Sequence 132, App
64	27	40.3	12	US-10-645-784-143	Sequence 143, App
65	27	40.3	12	US-10-645-784-144	Sequence 144, App
66	27	40.3	12	US-10-927-262A-17	Sequence 17, Appl
67	27	40.3	12	US-10-927-262A-24	Sequence 24, Appl
68	27	40.3	12	US-10-927-262A-25	Sequence 25, Appl
69	26	38.8	5	US-09-946-605-13	Sequence 13, Appl
70	26	38.8	5	US-10-014-716-13	Sequence 13, Appl
71	26	38.8	5	US-10-259-391-13	Sequence 13, Appl
72	26	38.8	5	US-10-190-951-13	Sequence 13, Appl
73	26	38.8	5	US-10-033-195B-12	Sequence 12, Appl
74	26	38.8	5	US-10-928-299-13	Sequence 13, Appl
75	26	38.8	5	US-10-966-767-13	Sequence 13, Appl
76	26	38.8	7	US-10-321-648-13	Sequence 12, Appl
77	26	38.8	7	US-10-387-957-36	Sequence 36, Appl
78	26	38.8	8	US-10-387-957-37	Sequence 37, Appl
79	26	38.8	8	US-10-387-957-38	Sequence 38, Appl
80	26	38.8	8	US-10-387-957-39	Sequence 39, Appl
81	26	38.8	8	US-10-387-934-36	Sequence 36, Appl
82	26	38.8	8	US-10-387-934-37	Sequence 37, Appl
83	26	38.8	8	US-10-387-934-38	Sequence 38, Appl
84	26	38.8	8	US-10-387-934-39	Sequence 39, Appl

85	26	38.8	8	16	US-10-387-955-36	Sequence 36, Appl
86	26	38.8	8	16	US-10-387-955-37	Sequence 37, Appl
87	26	38.8	8	16	US-10-387-955-38	Sequence 38, Appl
88	26	38.8	8	16	US-10-387-955-39	Sequence 39, Appl
89	26	38.8	8	16	US-10-488-219-36	Sequence 36, Appl
90	26	38.8	8	16	US-10-488-219-37	Sequence 37, Appl
91	26	38.8	8	16	US-10-488-219-38	Sequence 38, Appl
92	26	38.8	8	16	US-10-488-219-39	Sequence 39, Appl
93	26	38.8	10	10	US-09-900-590-66	Sequence 66, Appl
94	26	38.8	10	10	US-09-900-590-68	Sequence 68, Appl
95	26	38.8	10	10	US-09-750-754-74	Sequence 74, Appl
96	26	38.8	10	14	US-10-305-231-66	Sequence 66, Appl
97	26	38.8	10	14	US-10-305-231-98	Sequence 98, Appl
98	26	38.8	10	15	US-10-463-847-66	Sequence 66, Appl
99	26	38.8	10	15	US-10-463-847-98	Sequence 98, Appl
100	26	38.8	11	10	US-09-988-493-181	Sequence 181, Appl

ALIGNMENTS

RESULT 1
US-10-221-042-2
Sequence 2, Application US/10221042
Publication No. US20040120946A1
GENERAL INFORMATION:
APPLICANT: KANEKA CORPORATION
TITLE OF INVENTION: ADSORBENTS FOR DILATED CARDIOMYOPATHY
FILE REFERENCE: 12218/5
CURRENT APPLICATION NUMBER: US/10/221.042
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: PCT/JP01/03026
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: JP 2000-106915
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: peptide
NAME/KEY: MISC FEATURE
OTHER INFORMATION: Peptide having a binding affinity for an antibody against
OTHER INFORMATION: beta1-adrenoceptor and/or an antibody against M2 muscarinic recep
US-10-221-042-2

Query Match 50.7%; Score 34; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYGSFF 6
Db 1 EYGSFF 6

RESULT 2
US-08-424-550B-252
Sequence 252, Application US/08424550B
Publication No. US20020119447A1
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAM J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. EKKER
APPLICANT: SHERI L. BUIJK

APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AB6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-252

Query Match 50.7%; Score 34; DB 8; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.6e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 FSELMTS 12
Db 1 FSHLMTS 7

RESULT 3
US-09-214-371-35
Sequence 35, Application US/09214371B
Patent No. US2001001851A1
GENERAL INFORMATION:
APPLICANT: Lane, David
APPLICANT: Bottger, Volker
APPLICANT: Bottger, Angelica
APPLICANT: Picklesley, Stephen
APPLICANT: Chene, Patrick
APPLICANT: Hochkeppel, Heinz-Kurt
APPLICANT: Garcia-Echeverria, Carlos
APPLICANT: Purel, Pascal
TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
FILE REFERENCE: 4-20937/A/BCT
CURRENT APPLICATION NUMBER: US/09/214,371B
CURRENT FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:peptide
NAME/KEY: VARIANT
LOCATION: (1)

OTHER INFORMATION: X = Ac-Cys(Acrid)
 NAME/KEY: VARIANT
 LOCATION: (10)
 OTHER INFORMATION: X = Pro-NH2
 US-09-214-371-35

Query Match 44.8%; Score 30; DB 9; Length 10;
 Best Local Similarity 62.5%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GSFSELM 10
 DB 2 GPTFSDLM 9

RESULT 4
 US-09-214-371-36
 Sequence 36, Application US/09214371B
 Patent No. US20010018511A1
 GENERAL INFORMATION:
 APPLICANT: Lane, David
 APPLICANT: Botzger, Volker
 APPLICANT: Botzger, Angelica
 APPLICANT: Pickstey, Stephen
 APPLICANT: Chene, Patrick
 APPLICANT: Hochkeppel, Heinz-Kurt
 APPLICANT: Garcia-Echeverria, Carlos
 APPLICANT: Furel, Pascal
 TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
 FILE REFERENCE: 4-20937/A/PCT
 CURRENT APPLICATION NUMBER: US/09/214,371B
 PRIOR FILING DATE: 1999-03-26
 PRIOR APPLICATION NUMBER: PCT/EP97/03549
 NUMBER OF SEQ ID NOS: 83
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 36
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:peptide
 NAME/KEY: VARIANT
 LOCATION: (1)
 OTHER INFORMATION: X = Ac-Cys
 NAME/KEY: VARIANT
 LOCATION: (10)
 OTHER INFORMATION: X = Pro-NH2
 US-09-214-371-36

Query Match 44.8%; Score 30; DB 9; Length 10;
 Best Local Similarity 62.5%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GSFSELM 10
 DB 2 GPTFSDLM 9

RESULT 5
 US-09-900-590-100
 Sequence 100, Application US/09900590
 Publication No. US2003002809A1
 GENERAL INFORMATION:
 APPLICANT: Huse, William D.
 APPLICANT: Glaeser, Scott M.
 TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
 Antibodies, Nucleic Acids Encoding Same and Methods of Use
 NUMBER OF SEQUENCES: 100
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell & Flores LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego

STATE: California
 COUNTRY: United States
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/900,590
 FILING DATE: 06-Jul-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/016,061
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-IX 2965
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-9049
 INFORMATION FOR SEQ ID NO: 100:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 100:
 US-09-900-590-100

Query Match 44.8%; Score 30; DB 10; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGSFYS 7
 DB 5 YGSFYS 10

RESULT 6
 US-10-305-231-100
 Sequence 100, Application US/10305231
 Publication No. US2003016872A1
 GENERAL INFORMATION:
 APPLICANT: Huse, William D.
 APPLICANT: Wu, Herren
 TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
 Acids Encoding Same and Methods of Use
 FILE REFERENCE: P-IX 3536
 CURRENT APPLICATION NUMBER: US/10/305,231
 PRIOR FILING DATE: 2002-11-25
 PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US/09/339,922
 PRIOR FILING DATE: CURRENT FILING DATE: 1999-06-24
 NUMBER OF SEQ ID NOS: 112
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 100
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Mutated
 OTHER INFORMATION: complementarity determining region (CDR)
 US-10-305-231-100

Query Match 44.8%; Score 30; DB 14; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGSFYS 7
 DB 5 YGSFYS 10

```
RESULT 7
US-10-463-847-100
; Sequence 100, Application US/10463847
; Publication No. US2004006213A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
;           Glaeser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
;           Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/10/463,847
; FILING DATE: 16-Jun-2003
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-463-847-100

Query Match      44.8%; Score 30; DB 15; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      2 YGSFFS 7
Db      5 YGSFFS 10

RESULT 8
US-10-927-262A-35
; Sequence 35, Application US/10927262A
; Publication No. US20050137137A1
; GENERAL INFORMATION:
; APPLICANT: LANE, DAVID P
; APPLICANT: BOTTLER, VOLKER
; APPLICANT: BOTTLER, ANGELIKA
; APPLICANT: PICKSLEY, STEVEN M.
; APPLICANT: HOCHKEPPEL, HEINZ-KURT
; APPLICANT: GARCIA-ECHEVERRIA, CARLOS
; APPLICANT: CHENE, PATRICK
; APPLICANT: FURET, PASCAL
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN P53 AND MDM2
; FILE REFERENCE: 39749,0002 APC CON
; CURRENT APPLICATION NUMBER: US/10/927,262A
```

```
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: 09/214,371
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: GB 9614197.3
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: GB 9707041.1
; PRIOR FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Cys(Acrid)
US-10-927-262A-35

Query Match      44.8%; Score 30; DB 18; Length 10;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      3 GSFFSELM 10
Db      2 GSFFSELM 9

RESULT 9
US-10-927-262A-36
; Sequence 36, Application US/10927262A
; Publication No. US20050137137A1
; GENERAL INFORMATION:
; APPLICANT: LANE, DAVID P
; APPLICANT: BOTTLER, VOLKER
; APPLICANT: BOTTLER, ANGELIKA
; APPLICANT: PICKSLEY, STEVEN M.
; APPLICANT: HOCHKEPPEL, HEINZ-KURT
; APPLICANT: GARCIA-ECHEVERRIA, CARLOS
; APPLICANT: CHENE, PATRICK
; APPLICANT: FURET, PASCAL
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN P53 AND MDM2
; FILE REFERENCE: 39749,0002 APC CON
; CURRENT APPLICATION NUMBER: US/10/927,262A
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: 09/214,371
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: GB 9614197.3
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: GB 9707041.1
; PRIOR FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 36
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-927-262A-36

Query Match      44.8%; Score 30; DB 18; Length 10;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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OY 3 GSPFSELM 10
Db 2 GPTFSDLM 9

RESULT 10

US-10-858-271-10
; Sequence 10, Application US/10858271
; Publication No. US20040259829A1
; GENERAL INFORMATION:
; APPLICANT: Danks, Mary K.
; APPLICANT: Potter, Philip M.
; APPLICANT: Houghcon, Peter J.
; TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of
; TITLE OF INVENTION: Tumor Cells
; FILE REFERENCE: SU-0005
; CURRENT APPLICATION NUMBER: US/10/858,271
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US/09/595,682
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/075,258
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: PCT/US99/03171
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-858-271-10

Query Match 43.3%; Score 29; DB 16; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 4 SFPSELM 10
Db 1 AFWTELM 7

RESULT 11

US-10-659-207-28
; Sequence 28, Application US/10659207
; Publication No. US20050037959A1
; GENERAL INFORMATION:
; APPLICANT: CWIRLA, STEVEN E.
; APPLICANT: BALU, PALANI
; APPLICANT: DURFIN, DAVID J.
; APPLICANT: PIRLANI, SUNILA
; APPLICANT: MERRILL, BARBARA MCEOWEN
; APPLICANT: SCHATZ, PETER JOSEPH
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
; TITLE OF INVENTION: USES
; FILE REFERENCE: 0300-0014
; CURRENT APPLICATION NUMBER: US/10/659,207
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US/09/620,091
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-659-207-28

Query Match 43.3%; Score 29; DB 17; Length 10;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 4 SFPSELM 10
Db 3 SFWTELM 9

RESULT 12

US-09-486-734A-35
; Sequence 35, Application US/09486734A
; Patent No. US20020164732A1
; GENERAL INFORMATION:
; APPLICANT: Chopin, Marie-Christine
; APPLICANT: Clier, Florence
; APPLICANT: Erlich, S. Dusko
; APPLICANT: Gautier, Michel
; APPLICANT: Schouler, Catherine
; APPLICANT: Institut National de la Recherche Agronomique
; TITLE OF INVENTION: Resistance Mechanisms to Ic Type R/M
; TITLE OF INVENTION: Bacteriophages of Lactic Acid Bacteria
; FILE REFERENCE: 3339/196048
; CURRENT APPLICATION NUMBER: US/09/486,734A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/FR98/01873
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: FR 97/10885
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hsds subunit
US-09-486-734A-35

Query Match 41.8%; Score 28; DB 9; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.6e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 GSPFSEL 9
Db 2 GSFFXQL 8

RESULT 13

US-09-881-276-6
; Sequence 6, Application US/09881276
; Patent No. US20020031761A1
; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Payelle
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: DYX-009 0 US-2
; CURRENT APPLICATION NUMBER: US/09/881,276
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/669,271
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/186,958
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: parvovirus B19 binding polypep
US-09-881-276-6

Query Match 41.8%; Score 28; DB 9; Length 11;
Best Local Similarity 62.5%; Pred. No. 6.7e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 FFSLEMTS 12
|||
Db 1 FFCALWPS 8

QY 6 FFSLEW 10
|||
Db 2 FSDLM 6

Search completed: August 3, 2005, 19:03:29
Job time : 152 secs

RESULT 14
US-10-417-895A-56
; Sequence 56, Application US/10417895A
; Publication No. US20040033569A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; APPLICANT: Cappuccilli, Guido
; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
; FILE REFERENCE: 1551.2002-001
; CURRENT APPLICATION NUMBER: US/10/417, 895A
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,686
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variant peptide for third complementarity
; OTHER INFORMATION: determining region of Fv region of an
; OTHER INFORMATION: immunoglobulin
US-10-417-895A-56

Query Match 41.8%; Score 28; DB 15; Length 11;
Best Local Similarity 44.4%; Pred. No. 6.7e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 SFSLEMTS 12
|||
Db 1 SYSSSWS 9

RESULT 15
US-09-214-371-83
; Sequence 83, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Plicksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214, 371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide, amin
; OTHER INFORMATION: acid residues 18-23 of human p53
US-09-214-371-83

Query Match 40.3%; Score 27; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;